



## **Concurrent Drought Stress and Vascular Pathogen Infection Induce Common and Distinct Transcriptomic Responses in Chickpea**

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Chickpea (Cicer arietinum); the second largest legume grown worldwide is prone to drought and various pathogen infections. These drought and pathogen stresses often occur concurrently in the field conditions. However, the molecular events in response to that are largely unknown. The present study examines the transcriptome dynamics in chickpea plants exposed to a combination of water-deficit stress and Ralstonia solanacearum infection. R. solanacearum is a potential wilt disease causing pathogen in chickpea. Drought stressed chickpea plants were infected with this pathogen and the plants were allowed to experience progressive drought with 2 and 4 days of R. solanacearum infection called short duration stress (SD stresses) and long duration stress (LD stresses), respectively. Our study showed that R. solanacearum multiplication decreased under SD-combined stress compared to SDpathogen but there was no significant change in LD-combined stress compared to LD-pathogen. The microarray analysis during these conditions showed that 821 and 1039 differentially expressed genes (DEGs) were unique to SD- and LD-combined stresses, respectively, when compared with individual stress conditions. Three and fifteen genes were common among all the SD-stress treatments and LD-stress treatments, respectively. Genes involved in secondary cell wall biosynthesis, alkaloid biosynthesis, defense related proteins, and osmo-protectants were up-regulated during combined stress. The expression of genes involved in lignin and cellulose biosynthesis were specifically up-regulated in SD-combined, LD-combined, and LD-pathogen stress. A close transcriptomic association of LD-pathogen stress with SD-combined stress was observed in this study which indicates that R. solanacearum infection also exerts drought stress along with pathogen stress thus mimics combined stress effect. Furthermore the expression profiling of candidate genes using real-time quantitative PCR validated the microarray data. The study showed that down-regulation of defense-related genes during LD-combined stress resulted in an increased bacterial multiplication as compared to SD-combined stress. Overall, our study highlights a sub-set of DEGs uniquely expressed in response to combined stress, which serve as potential candidates for further functional characterization to delineate the molecular response of the plant to concurrent drought-pathogen stress.

Keywords: Ralstonia solanacearum, microarray, unique response, cellulose and lignin biosynthesis, combined stress, drought-pathogen stress, molecular response

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## INTRODUCTION

Chickpea (Cicer arietinum) is second largest cultivated legume crop in world. The crop is vulnerable to drought stress (Gaur et al., 2012) as well as to wilt diseases like Fusarium wilt caused by Fusarium oxysporum f. sp. ciceris (Nene et al., 2012). Under field conditions drought and pathogen stress often occurs simultaneously. Moreover, the combination of drought and pathogen stress has been noted to be devastating for growth and yield of crop plants (Olson et al., 1990; McElrone et al., 2001). These two stressors are noted for their influence on each other's interaction with plant, which might result in either negative or positive impact on the plants. Several studies in Arabidopsis, bean, grapevine have shown that drought stress makes the plant vulnerable to pathogen infection (McElrone et al., 2001; Mayek-Péreza et al., 2002; Mohr and Cahill, 2003; Prasch and Sonnewald, 2013). Conversely, reports also indicate that drought stress enhances the defense response of plants against pathogen (Achuo et al., 2006; Ramegowda et al., 2013; Hatmi et al., 2015). Pathogen infection has also been shown to alter the response of plants to water-deficit conditions. For example, wilt causing pathogens inhabit the xylem tissues, resulting in vascular dysfunction, and consequently causes a drought-like effect in plants (Douglas and MacHardy, 1981; Genin, 2010).

Overall, it is observed that the water deprivation induced during combined occurrence of drought and vascular pathogen infection increases the susceptibility of plants against pathogen as well as drought stress (McElrone et al., 2001; Kavak and Boydak, 2011; Choi et al., 2013; Ochola et al., 2015). Therefore it is important to understand the impact of combined stress and the cognate defense strategies adopted by plants to circumvent the concurrent onslaught of drought and vascular pathogen. However, the studies to understand the underlying molecular responses to combined drought and vascular pathogen are limited (Choi et al., 2013). At this juncture, in our present study we tried to dissect the molecular response of chickpea under combined drought and Ralstonia solanacearum infection. R. solanacearum is one of the most devastating wilt causing vascular pathogen having a broad host range and known to invade more than 200 different plants species (Genin, 2010). R. solanacearum colonizes xylem tissue and secretes massive amount of exopolysaccharides, which subsequently interrupts xylem function and leads to the wilting of the plant (Genin, 2010). R. solanacearum infection in chickpea was observed to result in a mild to severe disease symptoms which include yellowing, wilting and cell death; however, it was also observed that R. solanacearum does not provoke sudden plant death in leaf-inoculated plants (Sinha et al., 2016). The molecular responses of plants against R. solanacearum infection has been extensively studied (Hwang et al., 2011; Ishihara et al., 2012; Chen et al., 2014; Prasath et al., 2014; Zuluaga et al., 2015); however, so far no attempt has been made to understand the transcriptomic responses of plant to combined drought and R. solanacearum infection.

Recently, Sinha et al. (2016) showed that drought restricts the multiplication of *R. solanacearum* in chickpea which suggests that combined stress can induce robust defense responses in chickpea,

thus proposes the need to explore transcriptomic responses of chickpea under combined drought and *R. solanacearum* infection. Since *R. solanacearum* infection in chickpea causes disease symptoms after 6 days post infection (dpi) (Sinha et al., 2016), it has been hypothesized that *R. solanacearum* probably induces early and late defense responses at 2 and 4 dpi, respectively.

In the present study, transcriptomic responses of chickpea toward combined and individual *R. solanacearum* infection and drought stress was investigated using microarray at two time points namely short duration (SD) and long duration (LD). The transcriptomic changes induced during LD and SD combined stresses were categorized as unique (responses observed only during combined stress) and common (responses overlapping between individual and combined stresses) responses.

### MATERIALS AND METHODS

#### **Plant Material and Growth Conditions**

Chickpea plants (variety ICC 4958) were grown in pots (5 inches diameter and 5 inches height) containing 500 gm of 3:1 mixture (vol/vol) of air dried peat (Prakruthi Agri Coco peat Industries, Karnataka, India) and vermiculite (Keltech Energies Pvt Ltd., Maharashtra, India) in an environmentally controlled growth chamber (PGR15, Conviron, Winnipeg, MB, Canada) with diurnal cycle of 12-h-light/12-h-dark, 200  $\mu$ Em<sup>-2</sup>s<sup>-1</sup> photon flux intensity, 22°C temperature and 75% relative humidity. Pots were bottom irrigated every 2 days with half strength Hoagland's medium (**TS1094**, Hi-media Laboratories, Mumbai, India).

## Inoculum Preparation for Pathogen Infection

*Ralstonia solanacearum* procured from Indian Type Culture Collection (ITCC# BI0001), IARI, New Delhi, India was grown in LB medium (without antibiotic) at 28°C to  $OD_{600} = 0.6$  with a continuous shaking of 200 rpm for 2.5 h. Culture was pellet down by centrifuging at 3500 × g for 10 min, washed thrice with sterile distilled water, and re-suspended in sterile distilled water to  $OD_{600} = 0.005$  corresponding to 7 × 10<sup>5</sup> colony forming units (cfu)/ml.

#### **Stress Treatments**

Pathogen stresses namely SD-pathogen (2 days post *R. solanacearum* infection) and LD-pathogen (4 days post *R. solanacearum* infection) and drought stress namely SD-drought, SD or fast drought imposition and LD-drought, LD or slow drought imposition were used for this study. The two drought methods were included with incite that duration of drought imposition determines the plant's biochemical and molecular responses and therefore may affect the combined stress outcome. With SD- and LD-drought and SD- and LD-pathogen stresses, two combinations of combined stress treatments namely SD-combined (fast drought with 2 days of *R. solanacearum* infection) and LD-combined stress (slow drought with 4 days of *R. solanacearum* infection) were considered. Altogether, six

stress treatments were SD-combined (SD drought stress with 2 days of *R. solanacearum* infection), SD-pathogen (2 days of *R. solanacearum* infection), SD-drought [SD drought stress, 35% field capacity (FC)], LD-combined (LD drought with 4 days of *R. solanacearum* infection), LD-pathogen (4 days of *R. solanacearum* infection) and LD-drought (30% FC). Four plants were maintained for each stress treatment, along with absolute control and mock control and were placed in growth chamber using completely randomized design (CRD).

Drought stress was imposed by withholding the water, and stress level was assessed by measuring pot mix using gravimetric method following Sinha et al. (2016). For SDand LD-drought stress treatments, water was withheld for 10 and 15 days for 29- and 24-day-old plants to attain 35% (SD-drought) and 30% FC (LD-drought), respectively, on 39th day of plant growth. R. solanacearum inoculation was done by vacuum infiltration, in which the plants were upturned in a beaker placed in vacuum chamber containing R. solanacearum culture (7  $\times$  10<sup>5</sup> cfu/ml) with 0.02% Silwet L77 (Lehle seeds, Fisher Scientific, Waltham, MA, USA) and vacuum of 8.7 psi was applied for 10 min. Plants were briefly rinsed instantly after infiltration. To avoid the entry of bacterial suspension into the pot mix, the pot surface was covered with polythene wrap prior to infiltration. R. solanacearum was infiltrated into 35- and 37-day-old plants and samples were collected after 4 and 2 days of infiltration for LD- and SD-pathogen stress treatments, respectively. In case of LDand SD-combined stress treatments, water was withheld for 8 and 11 days for 29- and 24-day-old plants to attain 40 and 35% FC, respectively. Following this, plants were vacuum infiltrated with 7  $\times$  10<sup>5</sup> cfu/ml of *R. solanacearum* culture and were allowed for 2 and 4 days of progressive drought stress post R. solanacearum infection. After 2 and 4 days of progressive drought stress, FC of SD- and LD-combined stressed plants were 35 and 30%, respectively. Since plants at 60% FC showed better growth than 100% FC because of the high water holding capacity of pot mix, absolute and mock controls were maintained at 60% FC. For mock control, plants were infiltrated with water containing 0.02% Silwet L77. Leaf samples for all the treatment were collected from 39 days old plant for microarray analysis. The methodology of stress imposition is diagrammatically illustrated in Supplementary Figure S2.

# Assessment of *In planta* Bacterial Numbers

Total *in planta* colony forming units (cfu) of *R. solanacearum* were counted at 0 and 2 days post treatment (dpt) for SD-pathogen and SD-combined stress, and at 0, 2, and 4 dpt for LD-pathogen and LD-combined stress experiments. The leaflets harvested from infiltrated plants were weighed and surface sterilized with 0.01%  $H_2O_2$  for 5 s and subsequently homogenized in 100  $\mu$ l of sterile water. After serial dilution in sterile water, leaflet homogenate was plated on LB medium without antibiotics. Since there was no significant difference in

dry weight (DW) as well as fresh weight (FW) ratio for individual pathogen and combined stressed plants, FW was accounted in calculating bacterial numbers. Bacterial count was expressed as log transformed values of cfu/mg FW of leaflet.

Cfu/mg was calculated using the following formula:

|        | = | Number of colonies $\times$ volume of homogenate (ml) $\times$ dilution factor |
|--------|---|--|
| CFU/mg |   | volume plated (ml)   |
|        |   | weight of the leaflet (mg)   |

#### **Relative Water Content**

For all the six stress treatments and controls, relative water content (RWC) was measured at the end of the experiment (39-day-old plant). Moreover, RWC was also measured for SD- and LD-drought at 8 and 11 days after start of drought imposition, respectively. To measure the RWC, FW of leaflet samples was measured immediately after sample collection and samples were hydrated by floating on de-ionized water. Turgid weight (TW) was noted once leaflets attended full turgidity after 6 h at 22°C temperature. Samples were then oven dried at 60°C until they reach constant weight after 3 days, and DW was measured. RWC was calculated using the formula:

$$RWC(\%) = \frac{FW - DW}{TW - DW} * 100$$

#### **Microarray Analysis**

Microarray analysis for all treatments was performed in two biological replicates after taking clue from previous studies with two biological replicates (Yang et al., 2012; Liu et al., 2014; Chan et al., 2016). Leaf samples from two plants were pooled to make one biological replicate following recommendation by Kendziorski et al. (2005). The pooled leaves were mixed properly and a part of it was used for RNA isolation. Customized chickpea microarray chip with 60 mer oligonucleotide probe (Agilent\_AMADID – 037094, Agilent technologies, Palo Alto, CA, USA) was used for the study. Entire experiment was performed once. The sampling method is thoroughly described in Supplementary Figure S3 and a flow chart describing the steps in the microarray analysis is shown in Supplementary Figure S4.

#### **RNA** Isolation

Total RNA from leaf tissue for all the treatments and controls was isolated using TRIzol reagent (Cat# 15596026, Invitrogen, Carlsbad, CA, USA) following manufacturers' protocol. Further, RNA was purified using RNeasy minikit (Cat# 74104, Qiagen, Hilden, Germany) and quantified using NanoDrop ND-1000 spectrophotometer (Thermo Scientific, Waltham, MA, USA). Quality of RNA was assessed on a Bioanalyzer (Agilent technologies, Palo Alto, CA, USA).

#### Labeling

Samples for transcriptome analysis were labeled using Agilent Quick-Amp labeling Kit (Cat# 5190-0442, Agilent Technologies, Palo Alto, CA, USA). Total RNA (RIN numbers 6–8, 500 ng) was reverse transcribed at 40°C using oligo(dT) primer tagged to a T7 polymerase promoter and converted to double stranded cDNA to be used as template for cRNA generation. cRNA was generated by *in vitro* transcription and the dye Cy3 CTP was incorporated during this step. The cDNA synthesis and *in vitro* transcription procedures were carried out at 40°C. Labeled cRNA was purified using Qiagen RNeasy columns (Cat# 74106, Qiagen, Hilden, Germany) and quality was assessed for yields and quality using the Nanodrop ND-1000.

#### Hybridization and Scanning

Labeled cRNA (600 ng) was fragmented at 60°C and hybridized on to a Chickpea GXP\_8X60K (AMADID: 037094) microarray chip. Fragmentation of labeled cRNA and hybridization were done using Gene Expression Hybridization Kit (Cat# 5190-0404, Agilent Technologies, California, USA). Hybridization was carried out in SureHyb Microarray Hybridization Chamber (Cat# G2534A, Agilent Technologies, Palo Alto, CA, USA) at 65°C for 16 h. The hybridized slides were washed with Agilent Gene Expression Wash Buffers (Cat# 5188-5327, Agilent technologies, Palo Alto, CA, USA) and scanned using the Agilent microarray scanner (Model# G2600D, Agilent Technologies, Palo Alto, CA, USA).

#### **Data Analysis**

Scanned images were quantified using Feature Extraction Software (Version-11.5 Agilent technologies, Palo Alto, CA, USA). Feature extracted raw data was analyzed using GeneSpring GX software (Version 12.1, Agilent technologies, Palo Alto, CA, USA). Normalization of the data was done in GeneSpring GX using the 50th percentile shift (where n has a range from 0 to 100 and n = 50 is the median) and differential expression patterns were identified for each sample. Fold expression values for combined stresses and pathogen stresses were obtained with respect to mock control and for drought stresses were obtained with respect to absolute control samples. Statistical unpaired student's t-test was applied among the replicates and p-value was calculated based on volcano plot algorithm (GeneSpring GX, Agilent technologies, Palo Alto, CA, USA). Microarray dataset was submitted to Gene Expression Omnibus (GSE89228). Differentially expressed genes (DEGs) with p-value < 0.05 were selected. Different fold change cut off values ranging from 0.5 to 1.5 were tried with intension of including genes with high fold change expression. Also we looked for the fold change value which did not eliminate genes related to hormone, biotic stress, abiotic stress and xylem modification. Consequently, upregulated genes with fold > 1 (log base2) and down-regulated genes with fold > -1 (log base2) were selected for further studies.

# Annotation of Transcripts and *In silico* Expression Profiling

Gene annotation data was retrieved from chickpea transcriptome database<sup>1</sup> (Verma et al., 2015). Further, annotation of some of the genes was updated by performing BLASTN search against chickpea database (taxid: 3827) available in NCBI. Differentially regulated genes were clustered using hierarchical clustering based on Pearson coefficient correlation algorithm<sup>2</sup>.

<sup>1</sup>http://www.nipgr.res.in/ctdb.html

Venn diagrams were generated to view the common and unique genes in various conditions (Venny 2.0<sup>3</sup>). Orthologous genes of *Arabidopsis thaliana* were obtained from chickpea transcriptome database<sup>4</sup> (Verma et al., 2015) and their GO enrichment was performed using AgriGO singular enrichment analysis<sup>5</sup> with default setting of Arabidopsis gene model (TAIR10) background and other parameters (statistical test method: Fisher; multitest adjustment method: Yekutieli FDR under dependency; significance level: 0.05<sup>5</sup>). Finally, heat maps were generated using GENE-E software<sup>6</sup>.

#### **Real-Time PCR Analysis**

RNA from leaf tissue (100 mg FW) was isolated by TRIzol reagent (Cat# 15596018, Thermo Fisher Scientific, Waltham, MA, USA) following manufacturer's guidelines. Quality, quantity and integrity of RNA were verified by agarose gel electrophoresis and NanoDrop (Thermo Scientific, Waltham, MA, USA). The RNA samples with O.D. ratios at 260/280 nm in the range of 1.9-2.1, and at 260/230 nm in the range of 2.0-2.3 were used for RT-qPCR. First strand cDNA was synthesized from 5 µg of DNase treated total RNA in a reaction volume of 50 µl using Verso cDNA synthesis kit (Cat# K1621, Thermo Fisher Scientific, Waltham, MA, USA). Primers were obtained from Sigma-Aldrich, St. Louis, MO, USA. Details of gene-specific primers used for the RT-qPCR are provided in Supplementary Table S1. Reaction mix was prepared by adding 1 µl of two fold-diluted cDNA and 1  $\mu$ l of each of the specific primers (10  $\mu$ M/ $\mu$ l) to 5  $\mu$ l of SYBR Green PCR master mix (Cat# 4309155, Thermo Fisher Scientific, Waltham, MA, USA) and final volume was made to 10 µl. The reaction was run in ABI Prism 7000 sequence detection system (Applied Biosystems, Foster City, CA, USA). Relative fold change in gene expression was quantified using  $2^{-\Delta \Delta Ct}$  method (Livak and Schmittgen, 2001) using CaActin1 (EU529707.1) as endogenous control to normalize the data. For all the RT-qPCR experiments, three independent biological replicates and two technical replicates were included. For statistical analysis, the relative quantification value (RQ) was transformed to log<sub>2</sub> value and test of significance was performed by one sample *t*-test.

## RESULTS

#### Differential Transcriptomic Response of Chickpea under Combined and Individual Drought and *Ralstonia solanacearum* Stresses

To understand the transcriptomic responses of chickpea to combined drought and vascular pathogen *Ralstonia solanacearum*, combined stress experiments were conducted by imposing two levels of drought and pathogen stress. The study was conducted with two types of drought stress namely

<sup>&</sup>lt;sup>2</sup>https://software.broadinstitute.org/morpheus/

<sup>&</sup>lt;sup>3</sup>http://bioinfogp.cnb.csic.es/tools/venny/

<sup>&</sup>lt;sup>4</sup>http://www.nipgr.res.in/ctdb.html

<sup>&</sup>lt;sup>5</sup>http://bioinfo.cau.edu.cn/agriGO/analysis.php

<sup>&</sup>lt;sup>6</sup>http://www.broadinstitute.org/cancer/software/GENE-E/

SD drought or fast drought (SD-drought) and LD drought or slow drought (LD-drought) with the premise that duration and severity of drought stress determines the plants biochemical and molecular responses and therefore may differentially influence the combined stress response in chickpea. Two time points in R. solanacearum growth, i.e., 2 days post infiltration (dpi) (SDpathogen stress) and 4 dpi (LD-pathogen stress) were selected for the evaluation of transcriptomic response of chickpea against R. solanacearum. With the two types of drought stress and two time points of R. solanacearum multiplication, we imposed two types of combined stress namely SD (SD-combined stress, fast drought with 2 days post combined stress treatment, dpt) and LD (LD-combined stress, slow drought with 4 dpt) (Supplementary Figure S2A). Before initiating the combined stress study, R. solanacearum was first assessed for its pathogenicity in chickpea. It was found that at an infiltrated concentration of  $7 \times 10^5$  cfu/ml, R. solanacearum was multiplying in planta and caused disease symptoms varying from mild water soaked lesions and vellowing to severe cell death and wilting. Also, bacterial ooze was noticed from base of the leaflet (Supplementary Figure S1). In the present study, drought stress was observed to induce reduction in leaf RWC. LD-drought stress showed more reduction in leaf water, i.e., 64% RWC after 11 days of water-withholding compared to SD-drought stress after 8 days of water withholding, i.e., 75% RWC (Supplementary Figure S2D) indicating an increased severity of drought stress with increased drought duration. Plants exposed to SD drought (FC-35%) and LD drought (FC-30%) showed 73 and 52% RWC, respectively, compared to 86% RWC in control plants after 10 and 15 days of drought treatment, respectively. R. solanacearum infiltration resulted in water soaking leading to 86% RWC in SD-combined stressed and 87% RWC in LD-combined stressed plants which were close to those of SD-pathogen (86%) and LD-pathogen (83%) stressed plants after 2 and 4 days post combined stress treatment (Supplementary Figure S2E). Notable reduction in planta multiplication of R. solanacearum was observed under SD-combined stress compared to SD-pathogen stress (Supplementary Figure S2B). However, in planta bacterial count was unchanged under LD-combined stress compared to LD-pathogen stress treatments (Supplementary Figure S2C).

Transcriptomic alterations in chickpea plants challenged with combined drought and *R. solanacearum* stress (SD- and LD-combined) and individual drought (SD- and LD-drought) and *R. solanacearum* stress (SD- and LD-pathogen) were studied by microarray analysis. Microarray data was submitted to Gene Expression Omnibus (GEO# GSE89228). The DEGs (Log<sub>2</sub> FC  $\geq \pm 1$ ) under drought stress compared to absolute control, and under combined and pathogen stresses compared to mock control were screened using unpaired *t*-test ( $p \leq 0.05$ ). Putative annotation of DEGs were obtained from chickpea transcriptome database<sup>7</sup> (Verma et al., 2015) and also by homolog search using nucleotide BLAST<sup>8</sup> against chickpea (NCBI taxid: 3827) database. The DEGs for which putative annotation could not be obtained by BLASTN or BLASTX were termed as unannotated

DEGs (Supplementary Table S2). Under both SD-pathogen and LD-pathogen stress treatments, many genes involved in defense response (WRKY33, MAP KINASE 11, and DEFENSIN) were up-regulated. Similarly, under SD-drought and LD-drought stress treatments, genes involved in signaling, biosynthesis of abscisic acid (ABA) and osmo-protectants namely the genes encoding for LATE EMBRYOGENESIS ABUNDANT 5 (LEA5), LOW-TEMPERATURE-INDUCED 65 KDA PROTEIN were upregulated. Concordant with these observations, genes involved in both defense responses and abiotic stress tolerance (genes encoding for LEA and RESPIRATORY BURST OXIDASE HOMOLOG B) were differentially expressed in SD-combined and LD-combined stresses, which conforms to the nature of the stressors (Supplementary Figure S5 and File S1). The majority of top most up-regulated genes were belonging to stress responsive and cell wall modification categories under combined stress (Supplementary Figure S5 and File S1).

The number of up- and down-regulated genes under each stress condition is shown in Figure 1. The maximum numbers of DEGs were found in LD drought stress (1426 genes). Comparison of DEGs among SD stress treatments showed 821 genes (31.8%) out of 1011 genes to be uniquely up-regulated in response to SD-combined stress whereas, SD-combined stress treatment had 129 and 58 DEGs in common with the SD-pathogen and SD-drought stress, respectively (Figure 1B). Similarly, 1039 genes (31.5%) out of 1287 total DEGs were uniquely expressed under LD combined stress (Figure 1C). LD-combined stress and LD-drought stress had 102 DEGs in common, and both LD-combined and LD-pathogen had 131 genes in common (Figure 1C). The overlapping (common) and unique genes were also examined between SD-combined and LD-combined; SDdrought and LD-drought; SD-combined and LD-combined stress transcripts (Figures 1D-F). As a result a substantial variation in stress responsive transcriptome under SD-and LD-stresses was observed. The number of DEGs was more in LD stresses over SD stresses. For instance, number of DEGs under LD-pathogen was 841 compared to 594 under SD-pathogen stress treatment. Similarly, LD-drought stress treatment exhibited 1333 DEGs against 1111 DEGs under SD-drought stress. The LD-combined stress resulted in differential expression of 1196 genes over 959 DEGs under SD-combined stress. Each stress transcriptome had more number of unique DEGs and less number of common DEGs. LD-pathogen, LD-drought and LD-combined stress had 707, 1000, and 946 unique DEGs, respectively, as compared to 460, 778, and 709 unique DEGs in response to SD-pathogen, SDdrought and SD-combined stress, respectively. Moreover, very small percentages (10-15%) of genes were common between the respective SD and LD treatments (Figures 1D-F).

The overlapping genes showed differential expression under different stresses. A few common genes between LD combined and LD drought stress (genes encoding for LEA5, E3 UBIQUI TIN-PROTEIN LIGASE, PP2C37, INOSITOL 3 PHOSPHATASE SYNTHASE LIKE, and MATE EFFULUX FAMILY PROTEIN 5) had higher expression in LD-combined stress as compared to LD-drought stress. On the other hand, genes encoding for PATHOGENESIS RELATED (PR), DEFENSIN, PROTEIN TRRXL LIKE, and UDP-GLYCOSYLTRANSFERASE 73C2

<sup>&</sup>lt;sup>7</sup>http://www.nipgr.res.in/ctdb.html

<sup>&</sup>lt;sup>8</sup>https://blast.ncbi.nlm.nih.gov/Blast.cgi



(UGT73C2) proteins showed down-regulation in LD-combined stress as compared to their up-regulation in LD-pathogen stress. However, some of the down-regulated genes encoding for proteins in SD-pathogen stress like CYTOCHROME P450 734A1 (CYP734A1) and GTP BINDING PROTEIN 1 were induced in SD-combined stress (**Figure 2**). All the LD stress treatments (combined and individual) had 15 genes in common where four genes exhibited similar expression and 11 others exhibited tailored expression (**Figures 1B**, **2** and Supplementary File S5).

The results obtained from microarray were verified by real time qPCR analysis of 14 genes, which were up-regulated in SD-combined stress. The differential expression of genes noted from qPCR and microarray are represented in Figure 3 for the comparison. We also checked the expression of these 14 genes in other stress treatments to determine their relevance under other combined or individual stress treatments. We observed up-regulation of genes encoding CYTOCHROME C OXIDASE and RETICULIN OXIDASE LIKE under SDcombined, LD-combined and LD-pathogen stresses. Similarly, genes encoding CARVEOL DEHYDROGENASE and VICILLIN LIKE had a very high up-regulation under SD-combined, LDcombined and LD-pathogen stresses when compared to SD and LD drought treatments. BETA-GLUCOSIDASE 12 LIKE, ACETYLTRANSFERASE, PROLINE DEHYDROGENASE 2, and ASPARTYL PROTEASE 1 encoding genes exhibited high upregulation in both SD and LD combined stresses. DIRIGENT PROTEIN 22 and LACCASE 7 LIKE encoding genes had high expression under SD-combined, SD-pathogen and LD-pathogen stresses. Gene for VEIN PATTERNING 1 (VEP1) was equally upregulated in all treatments (Supplementary Figure S6). With the qPCR results we show that except VEP1, all other genes selected from SD-combined dataset were either specifically expressed or had higher expression under SD-combined stress, LD-combined stress and LD-pathogen stress treatments as compared to rest of the treatments.

We further categorized the DEGs under each stress treatments based on gene ontology (GO) using Arabidopsis orthologs of chickpea genes (Supplementary Table S3). Overall, we found enrichment of up-regulated DEGs (from all stress treatments) in GO biological processes like response to stimulus, biological regulation, metabolic process, developmental process, transport, signaling, reproduction, cell death, cell division, negative regulation of biological process. Up-regulated DEGs were enriched in GO molecular functions like catalytic activity, protein, ion and nucleic acid binding, and cellular components like membrane, cell wall and symplast (Figure 4). Furthermore, SD- and LD-pathogen stressed transcriptomes exhibited upregulated DEGs belonging to specific categories like 'response to wounding/chitin/salt stress' and 'response to jasmonic acid (JA) and ABA, while up-regulated DEGs under LDpathogen stress were also enriched under 'respiratory burst during defense response' and 'response to water deprivation' category (Supplementary Figure S7). These results indicate that R. solanacearum infected plants manifest pathogen mediated drought stress like symptoms and oxidative burst to combat the pathogen at high titer. The down-regulated DEGs under SD- and LD- pathogen stress showed enrichment in categories like carbohydrate transmembrane transporter activity, fatty acid biosynthetic process, coumarin biosynthetic process, SA mediated signaling, negative regulation of defense response, systemic acquired resistance (SAR) and regulation of meristem growth (Supplementary Figure S7). Up-regulated DEGs under SD- and LD-drought stress were enriched in categories like response to water deprivation, ABA stimulus, negative regulation of biological process, cellular polysaccharide biosynthetic process whereas LD-drought treatment also showed enrichment in plasma membrane part, sugar and secondary active transporter activity and response to other organism categories. The downregulated genes under SD- and LD-drought were enriched with GO processes: such as plant hypersensitive response, response to biotic stimulus, SA biosynthetic process, negative regulation of PCD, negative regulation of defense response, SAR, ligand gated ion channel activity and positive regulation of flavonoid biosynthetic process (Supplementary Figure S7).

The up-regulated DEGs under SD-combined stress genes were enriched under GO categories: mitochondrial membrane part, phosphorylation, response to temperature stimulus and oxidative stress, oxidation of organic compound and glutamine family amino acid metabolic process, while up-regulated DEGs under LD-combined stress, were enriched in secondary cell wall (SCW) biogenesis, response to water deprivation, ABA stimulus, lipid metabolic process regulation, hyperosmotic salinity response, hormone mediated signaling, glucosinolate biosynthesis and defense response GO categories. Down-regulated genes under SD- and LD-combined stress were majorly enriched in inorganic anion transmembrane transporter activity, protein serine/threonine kinase activity, negative regulation of cell death, MAPKKK cascade, regulation of hypersensitive response, defense response to fungus, salicylic acid (SA) biosynthetic process, SAR and positive regulator of flavonoid biosynthetic process (Supplementary Figure S7).

#### Combined Stress and *R. solanacearum* Induces Transcriptome Changes Involved in Osmo-Protectant Accumulation

The genes involved in osmo-protectant biosynthesis, like those genes encoding for LEA, RAFFINOSE SYNTHASE, STACHYOSE SYNTHASE, VERBASCOSE SYNTHASE, DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHASE (P5CS), and PROLINE OXIDASE (involved in proline catabolism) were upregulated in SD and LD-drought and SD and LD combined stress treatments. Moreover, the genes encoding RAFFINOSE BIOSYNTHESIS and LEA were also up-regulated in LDpathogen stress indicating R. solanacearum mediated drought stress in the chickpea plants. Therefore, R. solanacearum infection itself mimics a dual abiotic and biotic stress in chickpea (Supplementary Figure S8). Results on hierarchal clustering among different treatments (based on differential gene expression) revealed closeness of LD-pathogen with SDcombined stress (Supplementary Figure S9) substantiating that R. solanacearum infection exerts both drought and pathogen stress in chickpea.



**FIGURE 2 | Expression profile of DEGs common between combined and individual stresses.** The DEGs with more than one fold expression and p < 0.05 under SD treatments (SD-pathogen, SD-drought, SD-combined stress) and LD treatments (LD-pathogen, LD-drought, LD-combined) were compared and DEGs common between combined and individual stresses were selected. The heat maps represent DEGs which are shared between combined and individual stresses but have at least one fold difference in their expression between two treatments. Heat map (**A**) represents 12 shared genes with differential expression out of total 129 common genes between SD-pathogen and SD-combined and (**B**) represents 16 out of total 58 shared genes between SD-drought and SD-combined stress with differential expression out of total 131 common genes between LD-pathogen and LD-combined and (**D**) represents 27 out of total 102 common genes between LD-drought and LD-combined stress. Expression level of DEGs common among all LD stresses are represented in heat map (**E**). Color scale shows gene expression range where color bar in red and blue represents up- and down-regulated genes, respectively. Details of the genes shown in heat maps are available in Supplementary File S5.



### Combined Stress Differentially Induces Genes Involved in Xylem Differentiation and Cellulose and Lignin Deposition

Differentially expressed genes in each stress category were mapped onto pathways involved in xylem differentiation based on available literature information (Růžička et al., 2015; Rybel et al., 2016). During SD-combined stress, we observed downregulation of the gene KANADI (one clade of the GARP family of transcription factors) that act as negative regulator of procambium/cambium and vascular tissue formation (Růžička et al., 2015; Rybel et al., 2016). KANADI also indirectly suppresses expression of HD-ZIPIII transcription factor which promotes meristem function and xylem tissue formation (Růžička et al., 2015; Rybel et al., 2016). Down-regulation of KANADI thus enhances the possibility of either cambial proliferation or xylem trans-differentiation in SD-combined stressed plants. Another gene encoding PHLOEM INTERCALATED WITH XYLEM (PXY) receptor which is responsible for the BRASSINAZOLE-RESISTANT 1 (BES) mediated signaling (Růžička et al., 2015; Rybel et al., 2016) was up-regulated in SD-combined stressed plants (Figure 5, Supplementary Figure S10 and File S2). This may result either in increased cambial proliferation or xylem differentiation. Moreover, the mapping of DEGs onto pathway for SCW synthesis during xylem formation revealed high and unique up-regulation of gene encoding for SECONDARY WALL-ASSOCIATED NAC DOMAIN 2 (SND2), a tier 3 gene regulator in cellulose synthesis (Růžička et al., 2015; Taylor-Teeples et al., 2015) under SD-combined stress. However, genes encoding CELLULOSE SYNTHASE 8 (CESA 8), COBRA LIKE 2, and COBRA LIKE 4 which are directly involved in cellulose biosynthesis (Mcfarlane et al., 2014)

were not differentially expressed in SD-combined stress but were highly and uniquely up-regulated in LD-combined stress (Figure 5, Supplementary Figure S10). Among genes involved in lignin biosynthesis, the gene encoding for CINNAMYL-ALCOHOL DEHYDROGENASE 9 (CAD9) which catalyzes the terminal step of monolignol biosynthesis (Bonawitz and Chapple, 2010) showed high up-regulation under SD-combined and LD-pathogen stresses. Also, very high up-regulation of LACCASE7 which is involved in polymerization of monolignol to lignin (Bonawitz and Chapple, 2010) was observed in SD-combined and LD-pathogen stress. Similarly, LACCASE17 showed up-regulation in SD-combined, LD-combined and LDpathogen stresses. However, the genes involved in earlier steps of phenylpropanoid pathway for monolignol biosynthesis were down-regulated in both SD-combined and LD-combined stress (Figure 5, Supplementary Figures S10, S11, and File S3). The genes acting at later stage or regulating lignin polymerization were up-regulated under SD-combined, LD-combined, and LDpathogen stress. Therefore, we assume that genes involved in initial step of lignin synthesis (phenylpropanoid pathway) is up-regulated at early time point during combined stress for initiating lignin synthesis pathway and later may be downregulated to maintain the metabolic load. This could possibly be because of feedback regulation mediated by high monolignol titer in the cell at 2 and 4 dpi. PAL which catalyzes first step in phenylpropanoid pathway for lignin biosynthesis has been reported to work under sophisticated regulatory control. Both Pal activity and PAL gene transcription are negatively regulated by trans-cinnamic acid (t-CA) (Zhang and Liu, 2015). A transient induction in PAL gene expression has been observed in many studies. In A. thaliana, the expression of PAL1 and CAD genes upon Pseudomonas syringae pv. tomato DC3000 (Psd) infection had highest expression at 2 h post infection (hpi). However, PAL expression declined at 4 hpi and later time points, i.e., 8, 12, 24 hpi (Arabidopsis eFP Browser<sup>9</sup>). Schmelzer et al. (1989) reported a rapid and transient increase in PAL and 4CL mRNA level from 4 to 8 hpi followed by rapid decline in Parsley leaves upon Phytophthora megasperma f. sp. glycinea (Pmg) infection. The transient increase followed by decline in PAL activity at 12 h post R. solanacearum infection in resistant and 18-30 h post R. solanacearum infection in susceptible tomato variety was also reported by (Vanitha and Umesha, 2009). Kubasek et al. (1992) suggested that flavonoid genes are sequentially induced in the order of the biosynthetic steps in the flavonoid pathway and this level of regulation may be achieved by feed-forward or feedback mechanisms utilizing phenylpropanoid intermediates themselves. These evidences indirectly support our argument of sequential and transient expression of genes involved in lignin biosynthesis.

Hemi-cellulose deposition in cell wall is another important step in xylem biosynthesis. We observed up-regulation of gene *GLYCOGENIN-LIKE STARCH INITIATION 3 (PGSIP3)* also called GUX2 regulating hemi-cellulose biosynthesis (Mortimer et al., 2010) in only LD-pathogen stress. Whereas, the hemi-cellulose biosynthesis gene; *IRREGULAR XYLEM 15* 

<sup>&</sup>lt;sup>9</sup>http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi



DEGs in each treatment is mentioned in Supplementary Table S2.



**treatments.** Diagrams represent vascular bundle structure with phloem, cambium and xylem vessel/fiber and xylem parenchyma. The order of the cell in the diagram is likely following the order present in dicot leaf where phloem is placed on abaxial followed by cambium and xylem on adaxial surface. DEGs with minimum fold change 1 (Log<sub>2</sub> converted) were identified in each individual and combined stressed transcriptome over their respective controls. DEGs were mapped onto 'xylem development and SCW deposition' pathways based on literature information. Major molecular events related to xylem differentiation and SCW synthesis in xylem vessel, tracheary element and fiber are represented once in the same box. The SCW synthesis pathway is representing only those genes which are differentially expressed in the SD-combined and LD-combined stress transcriptome. Thickening of SCW in xylem vessel and TE are represented as thick green wall of the cell. Increased cellulose and lignin deposition in LD-combined stress is represented as dark thick green color wall. Genes in red boxes represents up-regulated expression. Genes in the boxes with the light blue color has no differential expression. Details of the genes in the boxes are mentioned in the Supplementary File S2.

(*IRX15*-like) (Brown et al., 2011) showed unique and high up-regulation in SD-combined stress only. Two hemicellulose biosynthetic genes encoding for PURVUS/GLZ1 and PECTIN METHYLESTERASE (PME) (Scheller and Ulvskov, 2010) were up-regulated during SD- and LD-drought stress, respectively (**Figure 5**, Supplementary Figures S10, S11 and Files S2, S3). This strongly suggests that combined stress results in induction of lignin biosynthesis and modification in xylem SCW.

Furthermore, we wanted to explore if up-regulation of genes involved in SCW formation is a general consensus under combined stress. Therefore we looked for the expression of genes encoding for CAFFEIC ACID O-METHYLTRANSFERASE (COAMT), LACCASE 7 and 17 and CESA7 and 8 genes in combined drought and Psd transcriptomic data from Gupta et al. (2016). We found absence of those genes in differentially expressed transcriptome of both drought first Psd later (DP) and Psd first and drought later (PD) treatments (Gupta et al., 2016) (Supplementary Figure S12). This indicates that combined drought and foliar pathogen stress may not employ SCW modification for combined stress tolerance.

#### Combined Drought and *R. solanacearum* Stress Differentially Induces Phytohormone Biosynthesis and Signaling Genes

The combined stress mediated alteration in hormone biosynthesis, catabolism, transport, and signaling were studied by mapping the DEGs onto hormone pathways based on available literature information. We found up-regulation of ABA biosynthesis genes in all stress treatments. We observed the stress treatment specific differential expression of ABA biosynthetic genes. ABA biosynthesis gene encoding 9-CIS-EPOXYCAROTENOID DIOXYGENASE 3 (NCED3) was specifically induced during SD- and LD-pathogen stress whereas during SD- and LD-drought stress, ABA biosynthetic genes encoding ZEAXANTHIN EPOXIDASE (ZEP) and NCED1 were induced. During SD-combined stress, ALDEHYDE OXIDASE (AAO) was specifically up-regulated, similarly in LD-combined stress only ZEP is found to be up-regulated. Down-regulation of gene encoding for ABA transporter ATP-BINDING CASSETTE G40 (ABCG40) was observed only during SD- and LD-drought. ABA receptor encoding genes were up-regulated in SD- and LD-pathogen stress and signaling genes PP2C6 and PP2C37 were up-regulated in SD-pathogen, SD-drought, LD-drought, and LD-combined stressed plants (Figure 6A and Supplementary File S4). PP2C is negative regulator of ABA signaling, however, has been shown to confer abiotic stress tolerance in many plants in ABA insensitive manner (Bhaskara et al., 2012; Zhang et al., 2013; Singh et al., 2015). Another negative regulator of ABA signaling geneABI5-interacting protein (AFP3) was also specifically up-regulated in LD-combined stress. The up-regulation of PP2C and AFP3 under drought stress has been previously reported (Garcia et al., 2008) but its role under combined stress has not been seen yet. These results indicate that ABA signaling plays a major part in plant response under drought, R. solanacearum and combined stress.

Short duration- and long duration-pathogen stresses in chickpea induced up-regulation of SA and ethylene (ET) signaling genes encoding for TGACG (TGA) MOTIF-BINDING PROTEIN 10 (TGA10), PATHOGENESIS-RELATED GENE, WRKY54, ETHYLENE RESPONSE FACTOR104 LIKE (ERF 104), and ERF1B (Figures 6B,D and Supplementary File S4). Contrastingly, we also encountered up-regulation of SA catabolism gene encoding for UDP-GLYCO-SYLTRANSFERASE 74 F1 (UGT74F1) in LD-pathogen stress. SD- and LD-pathogen stress in chickpea also induced upregulation of JA biosynthetic genes encoding ACYL-COA OXIDASE 1 and 2, respectively, but signaling genes were un-induced. SD-combined stress showed up-regulation of JA biosynthesis gene (OPCL1), down-regulation of SA repressor (PROTEIN TYROSINE PHOSPHATASE1 (PTP1), Bartels et al., 2009) and up-regulation of SA and ET signaling genes PR and MULTIPROTEIN BRIDGING FACTOR-1c (MBF1c), respectively (Figure 6C and Supplementary File S4). LD-combined stress treatment exhibited up-regulation of both JA biosynthetic genes OPCL1, AOS, and catabolism gene CYTOCHROM P450 94C1 (Figure 6C). While, LD-combined stress had upregulation of SA biosynthetic gene MES1 (METHYLESTE RASE 1), which converts methyl salicylate (MeSA) to SA (Dempsey et al., 2011), it showed down-regulation of SA signaling genes WRKY53, PR like, CBP60 and ET signaling genes MYB72 and ERF104 (Figures 6B,D). Altogether, they indicate toward suppression of immunity in LD combined stress (Supplementary Figure S13C). Collectively, our results on transcriptome analysis of phytohormone related genes suggest an involvement of ABA, SA, and ET mediated signaling in modulating combined stress response in these plants.

Both SD- and LD-combined stress showed up-regulation of brassinosteroid (BR) inactivator CYP734A1 (Vriet et al., 2013). Genes encoding for BR receptors BRASSINOSTEROID INSENSITIVE 1 (BRI1) and BRASSINOSTEROID INSENSI TIVE 1 LIKE 2 (BRI1like 2) were up-regulated under LD-combined and SD-pathogen stresses, respectively (Supplementary Figure S13B). LD-combined stress also showed up-regulation of gibberellin (GA) biosynthesis gene GIBBERELLIN 3-BETA-DIOXYGENASE 1 (GA1), catabolism gene CYTOCHROME P450 714ALIKE (CYP714Alike) and negative regulator of GA signaling gene; GIBBERELLIC ACID INSENSITIVE (GAI) indicating a loss of GA signaling in LD-combined stress (Supplementary Figure S13A). SD-combined stress resulted in up-regulation of genes encoding Auxin receptor; TOLL-INTERLEUKIN-RESISTANCE (TIR) and auxin transporter; ATP-BINDING CASSETTE B4 (ABCB4) (Supplementary Figures S13D and File S4).

#### Differential Expression of Defense Related Genes in SD- and LD-Combined Stress Influences *R. solanacearum* Multiplication

We looked for the differential expression of biotic stress responsive genes in the all the six treatments. We found upregulated expression of genes encoding PLEIOTROPIC DRUG



FIGURE 6 | Expression profile of hormone related genes in individual and combined stressed chickpea leaves. DEGs with minimum fold change 1 (Log<sub>2</sub> converted) were identified in each individual and combined stressed plants over their respective controls. DEGs were mapped onto 'hormone related' pathways using MAPMAN and KEGG softwares, literature and Arabidopsis hormone database (http://lifecenter.sgst.cn/orib/resourceDetail.do?resource.id=32682). Heat maps represent expression profile of hormone biosynthesis, catabolism, receptor, transport and signaling genes related to abscisic acid (A), salicylic acid (B), jasmonic acid (C), and ethylene (D) under individual and combined stresses. Fold change values (over respective controls) were used to plot heat maps where color bar in red and blue represents up- and down-regulated genes, respectively, and white represents no differential expression. Details are mentioned in the Supplementary File S4.

**RESISTANCE 3, ZINC FINGER PROTEIN, DOF ZINC FINGER** PROTEIN DOF1.1, SER/THR-PROTEIN KINASE EDR1, (STPKEDR1) RESPIRATORY BURST OXIDASE HOMOLOG B (RBOHB), TIR CLASS DISEASE RESISTANCE, and NITRATE REDUCTASE under SD-pathogen stress. LD-pathogen stress showed up-regulation of defense related genes encoding RETI CULIN OXIDASE LIKE PROTEIN, DISEASE RESISTANCE-RESPONSIVE (dirigent-like protein), GLUTAMINE AMIDO TRANSFERASE, PR, BOTRYTIS SUSCEPTIBLE 1, WRKY70, and RPP13. SD-combined stressed plants exhibited high upregulation of genes encoding RETICULIN OXIDASE LIKE PROTEIN (also called BERBERINE BRIDGE ENZYME) involved in alkaloid biosynthesis, DISEASE RESISTANCE-RESPONSIVE (DIRIGENT-LIKE PROTEIN), LACCASE 7 involved in lignan and antioxidant synthesis to confer defense response in plant (Figures 5, 7) (Dittrich and Kutchan, 1991; Zhao et al., 2013). SD-combined stress also exhibited high up-regulation of defense related genes encoding GLUTAMINE AMIDO TRANSFERASE, RBOHE like, STPK25, WRKY4, DOF5.4, and MAJOR LATEX PROTEIN LIKE 28 (MLP28) (Figure 7). SD-combined stressed transcriptome exhibited more number of up-regulated genes involved in defense response with high amplitude of expression as compared to SD-pathogen stress. This justifies the activated defense leading to decreased bacterial growth in SD-combined stress as compared to SD-pathogen. In LD-combined stress, we observed upregulation of genes encoding for RBOHE like, GLUTAMINE AMIDOTRANSFERASE C13C5.04, ZINC FINGER PROTEIN DOF5.4, CYS-RICH RECEPTOR KINASE 25, however, several defense related genes such as genes encoding DEFENSIN, MLO LIKE PROTEIN, BOTRYTIS-SUSCEPTIBLE1, PR5, CHITINASE, RETICULINE OXIDASE-LIKE, DIRIGENT-LIKE PROTEIN, WRKY12/47/33/31/35/75, RESISTANCE TO LEPTOSPHAERIA MACULANS 3 (RLM3), TIR-NBS-LRR FAMILY PROTEIN, SUPPRESSOR OF NPR1-1 (SNC4), and DISEASE RESISTANCE PROTEIN RPM1 were down-regulated which otherwise were up-regulated under either SD-pathogen, LD-pathogen or SD-combined stress (Figure 7). Therefore, we conclude that the imposition of slow drought has a different impact on defense related transcriptome and disease resistance capacity of plant when compared to fast drought.

### DISCUSSION

Xylem invading pathogens induce physiological drought stress in plants by blocking xylem and resultantly induce wilt (Genin, 2010). When wilt disease co-occurs with drought, plants are either resistant (Pennypacker et al., 1991; Sinha et al., 2016) or susceptible to the wilt pathogen (Abd El-Rahim et al., 1998; Choi et al., 2013). The combined occurrence of drought and vascular pathogen is often reported to reduce the plant height, total leaf area and decrease the hydraulic conductance, RWC and transpiration (Pennypacker et al., 1991; Abd El-Rahim et al., 1998; Choi et al., 2013). In our previous study (Sinha et al., 2016), the vascular pathogen *Ralstonia solanacearum* multiplication was shown to be significantly decreased after 6 days of infection under severe drought stress when compared to R. solanacearum infection alone in chickpea. In the present study, LD-combined stress did not change bacterial multiplication, however, SDcombined stress lead to decreased bacterial multiplication. The transcriptomic study under both SD- an LD-combined stresses unraveled responses unique to combined stress as well as responses common to both combined and individual stresses. Also SD- and LD-combined stress displayed very little overlap in transcriptomic responses between them which indicated that different durations of drought imposition in combined stress induces different transcriptomic changes in chickpea, consequently changing the overall effect on bacterial multiplication. Also, with increasing severity, the transcriptome complexity increased as reflected in more number of DEGs in LD-combined stress compared to SD-combined stress. Earlier, Gupta et al. (2016) reported increased resistance of A. thaliana to Psd under combined drought and Psd stress and they also reported that combined stress response differs with order of combined stress imposition (Gupta et al., 2016). However, Bidzinski et al. (2016) reported an increased susceptibility of rice plants toward Magnaporthe oryzae under intermittent drought and M. oryzae combined stress. Together these studies indicate that the plant's response toward combined stress varies with the severity and order of stresses and the plant's transcriptomic response also varies with continuous or intermittent drought stress. We also looked for the expression of certain unique genes from our study in transcriptomic data under combined drought and Psd (DPsd stress) stress in A. thaliana (Gupta et al., 2016) to compare if response to drought-foliar pathogen combination differs with drought-wilt pathogen combination. We could not find the differential expression of genes like LACCASE involved in lignin modification and flavonoid formation (Zhao et al., 2013) and CELLULOSE SYNTHASE involved in cellulose synthesis in DPsd transcriptome data. This suggests that unlike plant's response toward combined drought and wilt pathogen, combined stress with drought and foliar pathogen does not involve SCW modification. Gupta et al. (2016) suggested the priming of basal defenses due to interaction of drought and pathogen derived responses in combined stressed plants as a contributory factor for the resistance response observed under combined stress.

In the present study, we observed that R. solanacearum infection induces expression of genes involved in SA and ET signaling, biotic stress response and cell wall modification in chickpea. Earlier R. solanacearum infection to potato (Solanum commersonii) was also found to induce genes related to SA, ET, biotic stress and cell wall modification (Zuluaga et al., 2015). Narancio et al. (2013) also reported the R. solanacearum defense in potato (S. commersonii Dun) to be mediated by ET and SA mediated responses. They also reported up-regulation of ERF, PR, and WRKY genes. It was evident through transcriptome of LD-pathogen that R. solanacearum alone induces drought like symptoms. LD-pathogen stress showed highly up-regulated expression of genes encoding RAFFINOSE SYNTHASE, LEA14, MYOINOSITOL OXYGENASE, and CPRF2. The transcriptomic responses were close to SD-combined stress transcriptome indicating that chickpea upon R. solanacearum infection feels

| Α | SD-pathogen   | D | LD-pathogen   |
|---|---|---|---|
|   | TC27925 Breast cancer susceptibility protein 2  |   | TC33834 Reticuline oxidase-like protein   |
|   | TC00560 Ser/thr-protein kinase EDR1   |   | TC29559 Class 1 Glutamine amidotransferase  |
|   | TC01716 Respiratory burst oxidase E   |   | TC02279 Dirigent-like protein 22 like   |
|   | TC21397 PR homeodomain-like   |   | TC34554 Pathogenesis-related, PR  |
|   | TC23144 TIR class disease resistance  |   | TC17448 Cyclic dof factor 3-like  |
|   | TC05927 Nitrate reductase   |   | TC11727 Botrytis-susceptible1   |
|   | TC05331 WRKY 33   |   | TC04945 L type lectin kinase VII.2  |
|   | TC07333 WRKY 20   |   | TC10920 Cys-rich receptor-like kinase 25  |
|   | TC05894 Germin-like protein 3-2   |   | TC05027 Nitesta radiustana 2  |
|   | TC08360 MAP kinase kinase kinase  |   | TC26615 Auro/Cf.9 alicited 194  |
|   | TC25350 WRKY 12   |   | TC04818 Receptor protein kinase ZmPK1   |
|   | TC08518 Cys-rich receptor-like kinase 10  |   | TC03281 Disease resistance RPP13-like 3   |
|   | TC16083 Respiratory burst oxidase B like  |   | TC22770 L type lectin kinase  |
|   | TC08390 CC-NBS-LRR class protein  |   | TC14216 Ferredoxin-nitrite reductase  |
|   | TC27480 PEP1 receptor 2   |   | TC12715 Cyclic dof factor 2   |
|   | TC 17002 NB-ARC domain protein  |   | TC12412 Bax inhibitor 1   |
|   | TC0/069 STRUBBELIC recease (amily 2   |   | TC11743 bifunctional nuclease 1   |
|   | 1004808 STROBBELIG-receptor tarihiy S   |   | TC16561 MAC/perforin protein  |
|   |   |   | TC05115 Cys-nch receptor-like kinase 10   |
| В | SD-drought  |   | TC05894 Cormio-Eko protein 3-2  |
|   | TC14974 Glutamine amidotransferase  |   | TC12615 Polyketide cyclase  |
|   | TC24902 LRR and NB-ARC domains protein  |   | TC05117 Disease resistance protein RPM1   |
|   | TC29474 TIR-NBS-LRR protein   |   | TC14381 Tobamovirus multiplication-like   |
|   | TC34525 S-locus lectin kinase   |   | TC17002 NB-ARC domain containing  |
|   | TC07323 Cys, met, pro, gly protein 2, CMPG2   |   | TC01831 Cyclic nucleotide gated channel 10  |
|   | TC12020 Chitinase/PR4   |   | TC06616 NAC domain containing protein 42  |
|   | TC16992 WRKY70  |   | TC16635 G-type lectin S-receptor-like Kinase  |
|   | TC08390 CC-NBS-LRR class protein  |   | TC04968 STRUBBELIG-receptor family, SRF9  |
|   | TC07489 Ser/thre kinase, B120   |   | TC00633 TIR-NBS-LRR protein   |
| H | TC10373 ADR1-like 1   |   | TC22254 Receptor like protein 12  |
|   | TC10301 WRKY46  |   | TC12493 Recentor like protein 47  |
|   | TC06417 Jasmonate-ZIM-domain protein 1  |   | TC13030 RB receptor like STPK FLS2  |
|   | TC02937 LRR and NB-ARC domains protein  |   | TO TO SO THE TECEPTOLARE OT PA, TESE  |
|   | TC04061 WRKY17  |   |   |
|   | TC09651 PR thaumatin protein  | E | I D drought   |
|   | TC05630 WRKY11  | - | LD-urought  |
|   | TC00991 Receptor like protein 6   | - | TOT 1100 Obtamine and deterrations like   |
|   | TC17147 Tobacco hairpin-induced, HIN1   |   | TC14139 Glutamine amidotransferase like   |
|   | TC03281 NB-ARC domain   |   | TC08281 Cus.rich recentor-kinese 25   |
|   | TC22438 TIR-NBS-LRR protein   |   | TC31405 Kunitz trunsin/protanse inhibitor   |
|   | TC24938 Cytochrome P450 94B   |   | TC03400 R gene component  |
|   | TC04229 NBS domian protein  |   | TC00017 LRR and NB-ARC containing   |
|   | TC09416 WRKY1b  |   | TC10485 NB-ARC domain protein   |
|   | TC18913 Kunitz trypsin/protease inhibitor   |   | TC12050 Disease resistance RGA1   |
|   | TC14525 HS1 PRO-1 2   |   | TC29535 Endo-beta-glucanase 1-like  |
|   |   | - | TC20111 Resistance to Phakaasara pachurbizi 4   |
|   | TC09644 Dirigent-like protein   |   | 1020111 Resistance to Phatopsola pachymizi 4  |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein  |   | TC10761 WRKY 4  |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1   |   | TC10761 WRKY 4<br>TC10923 MAP kinase kinase 5-like  |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09893 Receptor like protein 48   |   | TC10761 WRKY 4<br>TC10923 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein  |
|   | TC09644 Dirigent-like protein<br>TC202522 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09893 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10  |   | TC10761 WRKY 4<br>TC10923 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase   |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Botrylis-suscepible 1<br>TC09693 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1   |   | TC10761 WRKY 4<br>TC10823 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC146572 Dynamin-related protein 1E  |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Butrytis-susceptible1<br>TC09989 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41   |   | Color H Neshado to Francisco a pacinima a<br>Colora I WRKY 4<br>TC10923 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nirrilase 2<br>C02037 Beasta Like SarChe kinase 10   |
|   | TC09644 Dirigent-like protein<br>TC29252 TI:NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC20989 Receptor like protein 48<br>TC21078 Cyclic nucleoside gated channel 10<br>TC21755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41  |   | CC0711 Nestada Carlandia Seria pechylniz a<br>TC10751 WRKY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Ntrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07249 Exc/Thr kinase 120  |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Bortytis-susceptible 1<br>TC099893 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC21755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br>SD-combined  |   | CC10761 WRRY 4<br>TC10623 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC07269 Demorin family cordein   |
| 0 | TC09644 Dirigent-like protein<br>TC29252 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14520 WRKY41<br>SD-combined  |   | CC10761 WRRY 4<br>TC10623 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-casted ion channel 2  |
| 0 | TC09644 Dirigent-like protein<br>TC02522 TIX-NIS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC20989 Receptor like protein 48<br>TC21078 Cyclic nucleoside gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br>SD-combined<br>TC07115 Vclin-like antinicrobial peptides   |   | CC0171 Hostace of Prancysol pechylniz a<br>TC10761 WRKY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC10338 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, 8120<br>TC17295 Remorin family protein<br>TC02946 Cyclic nucleotide-gated ion channel 2<br>TC026145 Cyclic in uccleotide-gated ion channel 2  |
| 0 | TC09644 Dirigent-like protein<br>TC02522 TIX-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09993 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC14520 WRKY41<br>SD-combined<br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reticuline oxidase-like<br>TC01942 Reticuline oxidase-like   |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC20237 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC10303 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26561 ADR 1-LIKE 1  |
| 0 | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC217955 Necrotic spotted lesions 1, NSL1<br>TC14520 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC09412 Recluine oxidase-like<br>TC34593 Dirigent-like protein 22<br>TC34593 Dirigent-like protein 22  |   | CC10761 WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC10261 WRRY 4<br>TC10233 TLR and NB-ARC domains protein<br>TC14652 Dynamin-related protein 1E<br>TC11033 Nitrlase 2<br>TC10371 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-cytled ion channel 2<br>TC28148 Cys-rich receptor-kinase 7<br>TC05951 ADR1-LIKE 1<br>TC05921 ADR1-LIKE 1   |
|   | TC09644 Dirigent-like protein<br>TC02522 TIX-NISS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC20989 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br>SD-combined<br>TC01912 Reticuline oxidase-like<br>TC01912 Reticuline oxidase-like<br>TC02412 Dirigent-like protein 22<br>TC29559 Glutamine amidotransferase<br>TC02512 Cyclochrome ad58 20  |   | CC10761 WRRY 4<br>TC10623 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC1033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC07499 Ser/Thr kinase, B120<br>TC022906 Cyclic nucleotide-gated ion channel 2<br>TC26561 ADR1-LIKE 1<br>TC05551 ADR1-LIKE 1<br>TC05921 ATP alpha hydrolases-like<br>TC0393 NC-NBS-LRR class protein  |
| c | TC09644 Dirigent-like protein<br>TC02522 TIX-NBS-LRR protein<br>TC20071 Botrytis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Nectrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Retouline oxidase-like<br>TC34531 Dirigent-like protein 22<br>TC34531 Dirigent-like protein 22<br>TC34531 Cyclotrome p450 82C<br>TC14851 NDR1/INI11-like, 1NHL1  |   | CC10761 WRRY 4<br>TC10623 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nirilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02966 Sycilic nucleotide-gated ion channel 2<br>TC05561 ADC(ici nucleotide-gated ion channel 2<br>TC05561 ADC1-LIKE 1<br>TC05921 ATP alpha hydrolases-like<br>TC08920 C-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein  |
|   | TC09644 Dirigent-like protein<br>TC02522 TIK-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC21078 Cytic nucleotide gated channel 10<br>TC21078 Cytic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC04921 Botuine oxidas-like<br>TC34213 Dirigent-like protein 22<br>TC29599 Glutamine amidotransferase<br>TC045171 Cytochrome p450 82C<br>TC18851 NDR1/HIN1-like 1, NHL1<br>TC01176 Respiratory burst oxidase E like   |   | CIG0761 WRRY 4<br>TC (10823 MAP kinase kinase 5-like<br>TC (2023) TLR and NB-ARC domains protein<br>TC (14699 IMP dehydrogenase/GMP reductase<br>TC (16572 Dynamin-related protein 1E<br>TC (1033 Nitrilase 2<br>TC (1033 Nitrilase 2<br>TC (17295 Remorin Tamily protein<br>TC (17995) ADR 1-LIKE 1<br>TC (17992) ADR 1-LIKE 1<br>TC (   |
| c | TC09644 Dirigent-like protein<br>TC02522 TIX-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC14755 Necrotic spotted lesions 1, NSL1<br>TC14520 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reloculine oxidase-like<br>TC04521 Dirigent-like protein 22<br>TC04521 Cytochrome p450 82C<br>TC14851 NDR1/INI1-like 1, NHL1<br>TC01916 Respiratory burst oxidase 25  |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC146899 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remoin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC05561 ADR-1L/KE 1<br>TC09291 ATP alpha hydrolases-like<br>TC0391 ATP alpha hydrolases-like<br>TC03930 CNBS-LRR class protein<br>TC31264 TIR-NBS-LRR class protein<br>TC31264 TIR-NBS-LRR class protein<br>TC31264 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC   |
| c | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC20787 Qctic nucleokide gated channel 10<br>TC217875 Necrotic spotted lesions 1, NSL1<br>TC14520 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC09142 Reticuline oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC24559 Glutamine amiddransferase<br>TC04512 Cytochrome p450 82C<br>TC18851 NDR 1/HIN1-like 1, NHL1<br>TC109176 Respiratory burst oxidase E like<br>TC192059 Glutomer p450 8881  |   | CC10761 WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02331 KAR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC10303 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC29561 ADQ16 nucleotide-gated ion channel 2<br>TC05561 ADQ16 nucleotide-gated ion channel 2<br>TC05561 ADQ16 nucleotide-gated ion channel 2<br>TC05561 ADQ11-LIKE 1<br>TC05290 TAP labra thydrolases-like<br>TC03208 Uncleotide case protein<br>TC32164 TR-NSS-LRR class protein<br>TC01298 Disease resistance protein RGA4<br>TC03210 URXY 46<br>TC03281 Disease resistance RPP13-like 3  |
| c | TC09644 Dirigent-like protein<br>TC02522 TIR-NIS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC209893 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC07115 Vicilin-like antimicrobial peptides<br>TC07115 Vicilin-like antimicrobial peptides<br>TC07115 Vicilin-like antimicrobial peptides<br>TC07115 Vicilin-like antimicrobial peptides<br>TC04571 Cyclochrome p450 826<br>TC18851 NDR1/HIN1-like 1, NHL1<br>TC107167 Respiratory burst coldase E like<br>TC071920 Sertith protein kinase 25<br>TC215854 Cyclochrome p450 83B1<br>TC295954 WRKY transcription factor 14   |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC07499 Ser/Thr kinase, B120<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26361 ADR1-LIKE 1<br>TC05561 ADR1-LIKE 1<br>TC05591 ATP alpha hydrolases-like<br>TC03900 CXIBS-LIR class protein<br>TC32164 TIR-NBS-LIR class protein<br>TC323164 TIR-NBS-LIR class protein<br>TC323164 TIR-NBS-LIR class protein<br>TC32364 TIR-NBS-LIR class protein<br>TC32364 TIR-NBS-LIR class protein<br>TC32464 TIR-NBS-LIR class protein<br>TC324764 TIR-NBS-LIR class protein<br>TC325764 TIR-NBS-LIR class protein<br>TC324764 TIR-NBS-LIR class protein<br>TC324764 TIR-NBS-LIR class protein<br>TC325764 TIR-NBS-LIR class protein<br>TC32577777777777777777777777777777  |
| c | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC20797 Cyclic nucleotide gated channel 10<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Nectoric spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC04512 Dirigent-like protein 22<br>TC24529 Glutuine oxidase-like<br>TC24529 Glutuine oxidase-like<br>TC24521 Cyclorhome p450 82C<br>TC18851 NDR1/INI1-like 1, NHL1<br>TC10920 Seritari protein inase 25<br>TC21546 Cytochrome p450 82H<br>TC09968 WRKY ranse z5  |   | CC10761 WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Sen/Thr kinase 10<br>TC07489 Sen/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Dyclic nucleotide-gated ion channel 2<br>TC05561 AD2(clic nucleotide-gated ion channel 2<br>TC05561 AD2(clic nucleotide-gated ion channel 2<br>TC05561 AD71-LIKE 1<br>TC09201 ATP alpha hydrolases-like<br>TC08390 CC-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC01298 Disease resistance protein RGA4<br>TC01301 WRRY 46<br>TC03281 Disease resistance RPP13-like 3<br>TC00758 G-type lectin S-receptor kinase<br>TC05355 SatI-inducible zinc finger 2<br>TC06416 WRY 45   |
| C | TC09644 Dirigent-like protein<br>TC02522 TIK-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC209803 Receptor like protein 48<br>TC21078 Cyclic nucleokide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC04912 Refcuine oxidas-like<br>TC34213 Dirigent-like protein 22<br>TC2959 Glutamine amidotransferase<br>TC04511 Cychorme p450 82C<br>TC18851 NDR1/HIN1-like 1, NHL1<br>TC01196 Refchorme p450 83B1<br>TC091965 WRKY transcription factor 14<br>TC019141 Zinc finger protein DCF5.4like<br>TC27736 L hype Locin kinase S.1-like  |   | Control Hostination of Handpisot pactified a<br>TC 10761 WRKY 4<br>TC 10223 MAP kinase kinase 5-like<br>TC 10233 ILR and NB-ARC domains protein<br>TC 14669 IMP dehydrogenase/GMP reductase<br>TC 16572 Dynamin-related protein 1E<br>TC 1033 Nitrilase 2<br>TC 0371 Receptor-like Ser/Thr kinase 10<br>TC 07499 Ser/Thr kinase, B120<br>TC 07499 Ser/Thr kinase, B120<br>TC 17295 Remorin family protein<br>TC 02906 Cyclic nucleotide-gated ion channel 2<br>TC 026561 ADR 1-LIKE 1<br>TC 09291 ATP alpha hydrolases-like<br>TC 02830 ADR 1-LIKE 1<br>TC 029201 ATP alpha hydrolases-like<br>TC 02830 ADR 1-LIKE 1<br>TC 029201 ATP alpha hydrolases-like<br>TC 02930 Bisease resistance protein<br>TC 02128 Disease resistance protein RGA4<br>TC 10330 WRKY 46<br>TC 00530 G-Hype lectin S-receptor kinase<br>TC 00530 G-Hype lectin S-receptor kinase  |
| C | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC20071 Botrytis-susceptible1<br>TC096933 Receptor like protein 48<br>TC21079 Cyclic nucleoside gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Viclin-like antimicrobial peptides<br>TC01942 Reticuline oxidase-like<br>TC3451 Dirigent-like protein 22<br>TC34531 Dirigent-like protein 22<br>TC34531 Okinamine amidotransferase<br>TC04571 Cytochrome p450 82C<br>TC1982 Neth/ININ-like 1, NHL1<br>TC19920 Serth/ININ-like 1, NHL1<br>TC19920 Serth protein Nase 25<br>TC21584 Cytochrome p450 83B1<br>TC09855 WRKY transcription Eator 14<br>TC17114 Zine finger protein TCF-Like<br>TC277361 Lybe lechin kinase 5 Like<br>TC277382 Lybe lechin kinase 5 Like   |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17285 Remoin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC05561 ADR1-LIKE 1<br>TC092901 ATP alpha hydrolases-like<br>TC03901 RC148C L<br>TC03501 CANBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC01298 Disease resistance protein RGA4<br>TC003551 Suppressor OF npr1-1; SNC1<br>TC09416 WRRY 31<br>TC29348 Suppressor OF npr1-1; SNC1   |
| C | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC20785 Qtrick uncleokide gated channel 10<br>TC21078 Cyclic nucleokide gated channel 10<br>TC21795 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC07415 Vicilin-like antimicrobial peptides<br>TC04921 Retuine oxidase-like<br>TC34521 Qtrickine oxidase-like<br>TC34521 Qtrickine oxidase-like<br>TC34521 Qtrickine oxidase-like<br>TC34521 Qtrickine oxidase Like<br>TC01192 Retuine oxidase Like<br>TC01192 Retuine oxidase Like<br>TC01920 Ser/thr protein Kinase 25<br>TC015184 Cytochrome p450 820<br>TC01986 WRKY transcription factor 14<br>TC01986 WRKY transcription factor 14<br>TC272955 Busci cancer susceptibility protein 2<br>TC029857 Major latex protein 18 2   |   | Coordin Hostinaste for Hakopson pachylina a<br>TC 10761 WRKY 4<br>TC 10823 MAP kinase kinase 5-like<br>TC 10283 TLR and N8-ARC domains protein<br>TC 14689 IMP dehydrogenase/GMP reductase<br>TC 16572 Dynamin-related protein 1E<br>TC 1033 Nitrilase 2<br>TC 03071 Receptor-like Ser/Thr kinase 10<br>TC 07499 Ser/Thr kinase, B120<br>TC 07495 Ser/Thr kinase, B120<br>TC 07495 Ser/Thr kinase, B120<br>TC 07495 IADR 1-LIKE 1<br>TC 09291 ATP alpha hydrolases-like<br>TC 03380 CC-NBS-LRR class protein<br>TC 01280 Disease resistance protein RGA4<br>TC 10301 WRKY 46<br>TC 00310 WRKY 46<br>TC 00350 G-type lectin S-receptor kinase<br>TC 00535 G-type lectin S-receptor kinase<br>TC 00545 G-type lectin S-receptor kinase<br>TC 00545 G-type lectin S-receptor kinase<br>TC 00555 G-type lectin S-   |
| 0 | TC09644 Dirigent-like protein<br>TC02522 TIX-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleoside gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reloculine oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC3453 Oktoheme antimicrobial peptides<br>TC04517 Cytochrome p450 82C<br>TC18851 NDR1/NIN1-like 1, NHL1<br>TC019716 Respiratory burst oxidase Elike<br>TC19920 Serth protein Nase 25<br>TC21584 Cytochrome p450 83B1<br>TC09985 WRKY transcription Factor 14<br>TC17114 Zine finger protein DCF5-Like<br>TC27736 L type lectin kinase 5. Like<br>TC29259 Braast cancer susceptibility protein 2<br>TC08985 WRKY transcription like 28<br>TC049845 L type lectin kinase VII.2   |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14689 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03701 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC02931 ATP alpha hydrolases-like<br>TC03931 RC0453 LR class protein<br>TC02930 CNBS-LRR class protein<br>TC02936 CNBS-LRR class protein<br>TC021280 Exease resistance protein RGA4<br>TC03031 WRRY 46<br>TC03281 Disease resistance protein RGA4<br>TC0305 Salt-inducible zinc finger 2<br>TC09416 WRRY 31<br>TC22438 Suppressor OF npr1-1; SNC1<br>TC0991 RCeptor like protein 6<br>TC0991 Receptor like protein 6  |
| C | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC29071 Botrylis-susceptible1<br>TC20795 Qicki nucleokide gated channel 10<br>TC217975 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Viclin-like antimicrobial peptides<br>TC074151 Viclin-like antimicrobial peptides<br>TC04421 Dirigent-like protein 22<br>TC24526 Qickuline oxidase-like<br>TC34521 Qickohome p450 82C<br>TC18851 NDR1HINI Like 1, NHL1<br>TC01916 Respiratory burst oxidase E like<br>TC01912 Retormer p450 83C<br>TC19142 Retormer p450 83C<br>TC19142 Catchomer p450 83C<br>TC19142 Gickohomer p450 83C<br>TC19141 Zinc Inger protein D75 4-like<br>TC27925 Bleast cancer susceptiblity protein 2<br>TC29259 Gicka cancer susceptiblity protein 2<br>TC09867 Major latex protein fike 28<br>TC09867 Major latex protein fike 28<br>TC049865 YMRV ranscription factor 14<br>TC19144 Zinc lectin kinase VII.2  |   | C10761 WRKY 4<br>TC10823 MAP kinase kinase 5-like<br>TC10761 WRKY 4<br>TC10823 MAP kinase kinase 5-like<br>TC10872 WRKY 4<br>TC10823 MAP kinase kinase 5-like<br>TC19233 Rikriase 2<br>TC1872 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC16720 Keceptor-like Ser/Thr kinase 10<br>TC07495 Ser/Thr kinase, B120<br>TC17205 Remorin Tamily protein<br>TC0206 Cyclic nucleotide-gated ion channel 2<br>TC026148 Cyc-ich receptor-kinase 7<br>TC05551 ADR1-LIKE 1<br>TC09291 ATP aiphe hydrolases-like<br>TC03206 Cyclic nucleotide-gated ion channel 2<br>TC0350 CC-NBS-LIR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC3250 Disease resistance protein RGA4<br>TC10301 WRKY 46<br>TC0303 Disease resistance RPP13-like 3<br>TC00758 G-type lectin S-receptor kinase finger 2<br>TC09916 WRKY 31<br>TC22438 Suppressor OF npr1-1, SNC1<br>TC09993 Receptor like protein 48<br>TC00991 Receptor like protein 48<br>TC00991 Receptor like protein 6<br>TC02444 MAC/Perforin domain protein<br>TC22438 Al-responsive montein ABR18.like   |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC01912 Reloculne oxidase-like<br>TC01912 Reloculne oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC3453 Unitarine amidicransferase<br>TC04571 Cytochrome p450 82C<br>TC18851 NDR1/HIN1-like 1, NHL1<br>TC019716 Respiratory burst oxidase 25<br>TC019542 Actochrome p450 83C<br>TC019542 Cytochrome p450 83B1<br>TC09956 WRKY transcription Factor 14<br>TC17114 Zine finger protein Tactor 14<br>TC27736L Lybe loctin kinase 25<br>TC04554 Cytochrome p450 83B1<br>TC09956 WRKY transcription Factor 14<br>TC17141 Zine finger protein Tactor 14<br>TC27736L Lybe loctin kinase VII.2<br>TC04854 SL type loctin kinase VII.2<br>TC11474 Tobacco hairpin-induced gene, HIN1<br>TC17842 Polykeide cyclase  |   | Control Hostinatoria of Prancipation pactification<br>Control Heart and NB-ARC domains protein<br>TC10283 LRR and NB-ARC domains protein<br>TC14689 IMP dehydrogenase/GMP reductase<br>C16572 Dynamin-related protein 1E<br>TC10303 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26261 Ago-rich receptor-kinase 7<br>TC05561 ADR-LIKE 1<br>TC029201 ATP alpha hydrolases-like<br>TC03930 Co-NBS-LRR class protein<br>TC023206 Cyclic nucleotide-gated ion channel 2<br>TC32514 TIR-NBS-LLR class protein<br>TC023201 Eases resistance RPP13-like 3<br>TC03291 Co-NBS-LRR class protein<br>TC03281 Cinesase resistance RPP13-like 3<br>TC03291 Stype lectin S-receptor kinase<br>TC0593 G4/pel lectin S-receptor kinase<br>TC05931 WRKY 46<br>TC03291 Disease resistance RPP13-like 3<br>TC09416 WRKY 31<br>TC22438 Suppressor OF npr1-1, SNC1<br>TC0991 Receptor like protein 6<br>TC00444 MAC/Perforin domain protein<br>TC0330 ABA-responsive protein ABR18-like   |
|   | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC2071 Botrytis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reticuline oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC3453 Oktohemine amiddransferase<br>TC04571 Cytochrome p450 82C<br>TC18851 NDR1/NIN1-like 1, NHL1<br>TC19920 Serline protein IA2<br>TC01992 Reticuline oxidase E like<br>TC09905 WRKY mass 25<br>TC21546 Cytochrome p450 82D<br>TC217114 Zine finger protein INase 25<br>TC21546 Cytochrome p450 83B1<br>TC29959 Gluch Initase 5.1-like<br>TC27925 Breast cancer susceptibility protein 2<br>TC09805 WIRKY mass cancer susceptibility protein 2<br>TC049851 Major latex protein like 28<br>TC17142 Zipkielde cyclase<br>TC17424 Polyeichid cyclase<br>TC08360 MK20id explase MapPiAA   |   | CitOffi WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02937 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC05561 ADR1-LIKE 1<br>TC09501 ADR1-LIKE 1<br>TC09309 Cyclic nucleotide-gated ion channel 2<br>TC05561 ADR1-LIKE 1<br>TC09309 Cyclic nucleotide spatel<br>TC03501 RADR1-LIKE 1<br>TC09309 Cyclic nucleotide spatel<br>TC03501 Kant Like 1<br>TC03501 Cyclic nucleotide spatel<br>TC03501 Kerker 1<br>TC032164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC032164 TIR-NBS-LRR class protein<br>TC03208 Disease resistance PT0418 TIR<br>TC23308 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein         TC02522 TIR-NBS-LRR protein         TC02652 TIR-NBS-LRR protein 48         TC09503 Receptor like protein 48         TC12075 Optic nucleoside gated channel 10         TC12755 Necrotic spotted lesions 1, NSL1         TC14520 WRV41         Stochastic spotted lesions 1, NSL1         TC14520 WRV41         TC01942 Reticuline oxidase-like         TC01942 Reticuline oxidase-like         TC01942 Reticuline oxidase-like         TC04520 TR1-like protein 22         TC2851 RC14NN1-like in, NHL1         TC01942 Reticuline oxidase-like         TC045371 Cytochrome p450 82C         TC11825 NBC14WY amscription factor 14         TC11920 Servity Transcription Factor 14         TC171942 Tbechrome p450 82C         TC27936 Lybe Icch ninase 25         TC3798 Lybe Icch ninase 25         TC34781 Lybe Icch ninase 5         TC34784 Lybe Icch ninase 5         TC3474 Tobaco haipini   |   | CitOffi WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC07499 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26148 Cys-rich receptor-kinase 7<br>TC05561 ADR1-LIKE 1<br>TC09291 ATP alpha hydrolases-like<br>TC03930 Cyclic nucleotide-gated ion channel 2<br>TC26144 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32301 WRKY 46<br>TC03301 WRKY 46<br>TC03305 Strinducible zistance RPP13-like 3<br>TC0758 G-type lectin 5-receptor kinase<br>TC05958 G-type lectin 5-receptor kinase<br>TC0598 G-type lectin 5-receptor kinase<br>TC0598 G-type lectin 5-receptor kinase<br>TC0598 G-type lectin 5-receptor kinase<br>TC0598 G-type lectin 5-receptor kinase<br>TC09898 Receptor like protein 48<br>TC00991 Receptor like protein 48<br>TC00944 McCPerforin domain protein<br>TC23308 ABA-responsive protein ABR18-like   |
| c | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC20071 Botrytis-susceptible1<br>TC096933 Receptor like protein 48<br>TC21079 Cyclic nucleoside gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Viclin-like antimicrobial peptides<br>TC01942 Reticuline oxidase-like<br>TC3451 Dirigent-like protein 22<br>TC3453 Dirigent-like protein 22<br>TC3453 ID Right-like antimicrobial peptides<br>TC04571 Cytochrome p450 82C<br>TC16851 NDR1/ININ-like 1, NHL1<br>TC10905 WRKY transcription stator 14<br>TC17145 Polyky transcription stator 14<br>TC17424 Divyky transcription stator 14<br>TC17442 Tokkeide cyclase<br>TC03360 MRC letch kinase 0.1-like 25<br>TC03458 Major latex protein like 28<br>TC03457 Major latex protein like 28<br>TC3735 MACiperforin domain-containing<br>TC03380 MRC putative kinase. MAP3KA   |   | CitOffi WRRY 4<br>TC1023 MAP kinase kinase 5-like<br>TC0233 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC03071 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC05561 ADR-LIKE 1<br>TC05561 ADR-LIKE 1<br>TC05591 ATP alpha hydrolases-like<br>TC03030 RC-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32810 Disease resistance protein RGA4<br>TC10301 WRKY 46<br>TC03281 Disease resistance protein RGA4<br>TC03505 Salt-inducible zinc finger 2<br>TC09416 WRKY 31<br>TC22438 Suppressor OF npr1-1; SNC1<br>TC09803 Receptor like protein 48<br>TC00991 Receptor like protein 48<br>TC00941 RCeptor like protein 48<br>TC00941 Receptor like protein 48<br>TC0308 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC21073 (2014: nullcolide gated channel 10<br>TC21073 (2014: nullcolide gated channel 10<br>TC21073 (2014: nullcolide gated channel 10<br>TC21735 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC0142 Reiculine oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC24559 Glutamine amiddorsanferase<br>TC04517 (2016-mme p450 82C<br>TC18851 NDR 1/I-IIN1-like 1, NHL1<br>TC01716 Respiratory burst oxidase E like<br>TC19142 Zirkichmer p450 82C<br>TC19142 Arbit protein kinase 25<br>TC19141 Zinc Inger protein DC54-like<br>TC27925 Breat cancer susceptibility protein 2<br>TC04959 (Juchomer p450 82C<br>TC19141 Zinc Inger protein DC54-like<br>TC27925 Breat cancer susceptibility protein 2<br>TC049451 Lybe lectin kinase 5.1-like<br>TC19442 Divisione lectin kinase VII.2<br>TC17442 Tobacco halipin-induced gene, HIN1<br>TC17424 Tobacco halipin-induced gene, HIN1<br>TC17825 Protein domain-containing<br>TC08338 Respiratory burst oxidase B like<br>TC03817 KMSC domain protein domain<br>TC16083 Respiratory burst oxidase B like<br>TC03817 KMSC domain protein RPM1   |   | Clorofe I WRKY 4<br>TC (1023) MRKY 4<br>TC (1023) MRKY 4<br>TC (1023) MRKY 4<br>TC (1023) MRKY 4<br>TC (1023) MRK and NB-ARC domains protein<br>TC (1469) MP dehydrogenase/GMP reductase<br>TC (123) MRC and Protein 1E<br>TC (1123) Miniase 2<br>TC (1225) Kenorin family protein<br>TC (1225) Kenorin family protein<br>TC (1225) Kenorin family protein<br>TC (125) Kenorin family f  |
| c | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC20071 Botrytis-susceptible1<br>TC029071 Botrytis-susceptible1<br>TC09893 Receptor like protein 48<br>TC14520 WRKY41<br><b>SD-combined</b><br>TC14520 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Retouline oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC34531 Dirigent-like protein 22<br>TC34531 Dirigent-like protein 22<br>TC34541 Dirigent-like protein 22<br>TC34541 Dirigent-like protein 22<br>TC34541 Dirigent-like protein 22<br>TC34542 Oxidonmine amidotransferase<br>TC04571 Cytochrome p450 82C<br>TC116851 NDR1/NIN1-like 1, NHL1<br>TC01716 Respiratory burst oxidase E like<br>TC09859 WRKY transcription Factor 14<br>TC17414 Zine finger protein InSec 25<br>TC04854 Lybe lectin kinase VII.2<br>TC17442 Polykatide cyclase<br>TC03430 MRC putative kinase MR-23KA<br>TC03830 MRC/patriot domain-containing<br>TC03830 MRC/patriot momain-containing<br>TC03857 LURP1-reliated protein domain<br>TC01117 NBS domain protein RPM11<br>TC11210 Faraid of VII.2  |   | Contractional Control of Plancy Society Securities and Control Transmission of Plancy Society Security 2017 Control Contrel Contrel Control Contection Control  |
| C | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC20718 Dortylis-susceptible1<br>TC20797 (Social Content of the protein 48<br>TC21078 (Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC04912 Reiculine oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC24559 (Buchune axidase-like<br>TC34513 Dirigent-like protein 22<br>TC24559 (Dirichline axidase-like<br>TC34513 Dirigent-like protein 22<br>TC3454 (Dirichline axidase-like<br>TC19428 NBC (Notherme p450 82C<br>TC11942 Reiculine oxidase E like<br>TC19863 NBC/11NIN-Like 1, NHL1<br>TC01916 Respiratory burst oxidase E like<br>TC19863 WRKY transcription factor 14<br>TC17114 Zine finger protein DC5 4.4ke<br>TC27925 Blesct ancer susceptiblity protein 2<br>TC04845 Lype lectin kinase 51-like<br>TC17424 Divedide cyclase<br>TC04359 MACyleation domain-containing<br>TC04380 Reparatory burst oxidase B like<br>TC03380 MRC putative kinase MAPSKA<br>TC25595 LURP1-related protein RM1<br>TC1142 Divedide Cyclase<br>TC19419 Paralog of NPR1<br>TC04985 TURP1-related protein RM1<br>TC12101 Paralog of NPR1  |   | Clorofi Trosharos of Prakopsol pachylhal a<br>TC10761 WRKY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02337 LRR and N8-ARC domains protein<br>TC14689 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02960 Cyclic nucleotide-gated ion channel 2<br>TC026148 Cyc-rich receptor-kinase 7<br>TC05551 ADR1-LIKE 1<br>TC02920 Cyclic nucleotide-gated ion channel 2<br>TC02921 ADR1-LIKE 1<br>TC02920 Cyclic nucleotide-gated ion channel 2<br>TC02921 ADR1-LIKE 1<br>TC02921 ADR1-LIKE 1<br>TC02921 ADR1-LIKE 1<br>TC02920 Cyclic nucleotide-gated ion channel 2<br>TC02921 ADR1-LIKE 1<br>TC02920 Cyclic nucleotide-gated ion channel 2<br>TC02941 Suppressor OF npr1-1; SNC1<br>TC02993 Receptor like protein 48<br>TC023300 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC20071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleoside gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reloculine oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC3453 Officianise amidicansferase<br>TC04511 Cytochrome p450 82C<br>TC18851 NDR1/NIN1-like 1, NHL1<br>TC019716 Respiratory burst oxidase E like<br>TC09859 Glutary transcription Factor 14<br>TC17147 Tobacco haripin-index 950 83B1<br>TC09985 WRX transcription Factor 14<br>TC17141 Zine finger protein IDCF5-Like<br>TC27595 Up lectin kinase VI.2<br>TC04851 Npt lectin kinase VI.2<br>TC04854 Lype lectin kinase VI.2<br>TC1487 Dbacco haripin-induced gene, HIN1<br>TC17147 Tobacco haripin-induced gene, HIN1<br>TC18030 MEX putative kinase, MAP3KA<br>TC28357 LURP1-reliated protein domain<br>TC04885 TLURP1-reliated protein domain<br>TC11807 Tbacs gratery protein TC1187<br>TC44885 TLURP1-reliated protein RPM1<br>TC1210P1 arrange of NPR1<br>TC04988 STRUBELIG-receptor family 3<br>TC44381 Tobacmavirus multiprication-like  |   | Control Hostinatoria of Prinko/Solo pachylina/ a<br>TC10761 WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02337 LRR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC103071 Receptor-like Ser/Thr kinase, 10<br>TC03701 Receptor-like Ser/Thr kinase, 10<br>TC07499 Ser/Thr kinase, 8120<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26361 ADR-14.IKC 1<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26361 ADR-14.IKC 1<br>TC03930 ICC NBS-LRR class protein<br>TC02901 ATP alpha hydrolases-like<br>TC03930 Co-NBS-LRR class protein<br>TC023261 Disease resistance RPP13-like 3<br>TC0310 WRRY 46<br>TC03281 Disease resistance RPP13-like 3<br>TC09416 WRRY 31<br>TC22438 Suppressor OF npr1-1, SNC1<br>TC09491 Receptor like protein 6<br>TC00441 McRY 46<br>TC00441 McRY 46   |
|   | TC09644 Dirigent-like protein<br>TC29252 TIK-NBS-LRR protein<br>TC20718 Dortylis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21078 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reticuline oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC24559 Glutanine amidotransferase<br>TC04517 Cyclochrome p450 82C<br>TC14851 NDR1/HIN1-like 1, NHL1<br>TC19982 WRKY transcription factor 14<br>TC19982 WRKY transcription factor 14<br>TC17114 Zine Inger protein DC5 4-like<br>TC27925 Bleast cancer susceptibility protein 2<br>TC049851 Michael cancer bildes<br>TC17142 Tobacco hairpin-induced gene, HIN1<br>TC17842 Polybeictin idomain-containing<br>TC08390 KRKy transcription factor 14<br>TC17442 Polybeictin idomain-containing<br>TC08390 KRK putative kinase MAP3KA<br>TC28557 MAC/perforin domain-containing<br>TC083917 MAC/perforin domain-containing<br>TC083917 MR2/partory burst oxidase B like<br>TC03517 NRS domain protein RM1<br>TC110420 Seriptiany burst oxidase B like<br>TC03517 NRS domain protein RM1<br>TC120498 STRUBBELIG-receptor famIk3<br>TC14381 Tobamovirus multiplication-like<br>TC32084 Cancer susceptor famIk3<br>TC14381 Tobamovirus multiplication-like  |   | Clorofi Hoshiado Charlos de Faladojski pachylinu a<br>TC 10761 WRKY 4<br>TC 10233 MAP kinase kinase 5-like<br>TC 102837 LRR and N8-ARC domains protein<br>TC 14699 IMP dehydrogenase/GMP reductase<br>TC 02371 Receptor-like Ser/Thr kinase 10<br>TC 037489 Ser/Thr kinase, B120<br>TC 07499 Ser/Thr kinase, B120<br>TC 07295 Cyclic nucleotide-gated ion channel 2<br>TC 026148 Cyclic nucleotide-gated ion channel 2<br>TC 026148 Cyclic nucleotide-gated ion channel 2<br>TC 026148 Cyclic nucleotide-gated ion channel 2<br>TC 026551 ADR1-LIKE 1<br>TC 028390 CC-NBS-LIRR class protein<br>TC 029201 ATP alpha hydrolases-like<br>TC 028300 CC-NBS-LIRR class protein<br>TC 021280 Disease resistance protein RGA4<br>TC 01280 Disease resistance protein RGA4<br>TC 00301 WRKY 46<br>TC 00301 WRKY 46<br>TC 00301 WRKY 41<br>TC 00398 Corport like protein 48<br>TC 00091 Receptor like protein 48<br>TC 00094 Receptor like protein 48<br>TC 00094 Receptor like protein 6<br>TC 00444 MAC/Perforin domain protein<br>TC 23308 ABA-responsive protein ABR18-like   |
| C | TC09644 Dirigent-like protein         TC02522 TIR-NBS-LRR protein         TC02622 TIR-NBS-LRR protein 48         TC09893 Receptor like protein 48         TC14520 WRKY41         Statesptor like protein 22         TC34513 Dirigent-like protein 24         TC34514 Cytochrome p450 83C         TC11475 Tbacco haripsi-indicator 14         TC17147 Tbacco haripsi-indicator 14         TC17147 Tbacco haripsi-indicade gene, HIN1         TC17147 Tbacco haripsi-indicade gene, HIN1         TC16935 MCK putative kinases MAPSKA         TC34351 Disgord NPX1         TC14381 Tback on haripsi-indicador admain-containing         TC14381 Tback on haripsi-indicador Hill         TC1147 Tback on haripsi-indicade gene, HIN1         TC1147 Tback on haripsi-indicade gene, HIN1         TC1120 Paragog INPR1         TC12088 STRUBE   |   | Citorfa I WRKY 4<br>TC10233 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC07298 Genr/Thr kinase, B120<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC02561 ADR-1LKE 1<br>TC09291 ATP alpha hydrolases-like<br>TC03501 ADR-1LKE 1<br>TC039201 CNBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC323164 TIR-NBS-LRR class protein<br>TC324164 TIR-NBS-LRR class protein<br>TC324164 TIR-NBS-LRR class protein<br>TC324164 TIR-NBS-LRR class protein<br>TC324164 TIR-NBS-LRR class protein<br>TC32300 NRKY 46<br>TC09918 Receptor like protein 48<br>TC00941 ACPerforin domain protein<br>TC32308 ABA-responsive protein ABR18-like   |
| C | TC09644 Dirigent-like protein<br>TC02522 TIR-NIS-LRR protein<br>TC2071 Botrytis-susceptible1<br>TC02652 TIR-NIS-LRR protein 48<br>TC21078 (cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Viclin-like antimicrobial peptides<br>TC01942 Retouline oxidase-like<br>TC34513 Dirigent-like protein 22<br>TC3453 Oktohemine amiddransferase<br>TC04517 (cyclochrome p450 82C<br>TC18851 NDR1/HIN1-like 1, NHL1<br>TC19925 Sefth/HIN1-like 1, NHL1<br>TC19925 Sefth/HIN1-like 1, NHL1<br>TC0995 WRKY transcription factor 14<br>TC27125 Ble cont hinase 25<br>TC21584 Cyclochrome p450 82B1<br>TC09955 WRKY transcription factor 14<br>TC17142 Polyket access cancer susceptibility protein 2<br>TC049851 Major latex protein like 28<br>TC034954 Lybe lectin kinase 5.1-like<br>TC17842 Polykeide cyclase<br>TC03800 MRC Justex protein like 28<br>TC03800 MRC Justex protein domain-containing<br>TC03800 MRC Justev VII.2<br>TC19141 TO40486 Lybe Justev MII.2<br>TC19141 TO40486 Lybe Justev Kinase ALI<br>TC03800 MRC Justev protein domain-containing<br>TC03807 MRC1 Justev Kinase ALI<br>TC03800 MRC Justev Kinase ALI<br>TC03800 MRC Justev Kinase MRP3KA<br>TC12825 TULRP1-related protein domain<br>TC12825 TULRP1-related protein domain<br>TC12825 TULRP1-related protein demain<br>TC12825 TULRP1-related protein domain<br>TC12825 TULRP1-r                       |   | C10761 WRKY 4<br>TC10823 MAP kinase kinase 5-like<br>TC10781 WRKY 4<br>TC10823 MAP kinase kinase 5-like<br>TC14657 Dynamin-related protein 1E<br>TC14030 Nitrilase 2<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC17295 Remorin Tamily protein<br>TC02060 Cyclic nucleotide-gated ion channel 2<br>TC026148 Cyc-ich receptor-kinase 7<br>TC05551 ADR1-LIKE 1<br>TC03206 Cyclic nucleotide-gated ion channel 2<br>TC03261 Kor-ich receptor-kinase 7<br>TC05551 ADR1-LIKE 1<br>TC03280 CC-NBS-LIRR class protein<br>TC32164 TIR-NBS-LIRR class protein<br>TC32164 TIR-NBS-LIRR class protein<br>TC32164 TIR-NBS-LIRR class protein<br>TC3250 Disease resistance protein RGA4<br>TC10301 WRKY 46<br>TC0303 Disease resistance RPP13-like 3<br>TC00758 G-type lectin S-receptor kinase<br>TC03993 Receptor like protein 48<br>TC00991 Receptor like protein 48<br>TC009146 WRKY 31<br>TC23308 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein<br>TC02525 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRV411<br><b>SD-combined</b><br>TC09451 Retruine avidase-like<br>TC01942 Reticuline oxidase-like<br>TC04511 Sveilin-like antimicrobial peptides<br>TC04521 Reticuline oxidase-like<br>TC34513 Dirigent-like protein 22<br>TC04551 Cytochrome p450 82C<br>TC01942 Reticuline amidcransferase<br>TC045511 Cytochrome p450 82C<br>TC01952 Strate Cytochrome p450 82C<br>TC01952 Strate Cytochrome p450 83C<br>TC09955 WRVY transcription Factor 14<br>TC19714 Zine finger protein factor 14<br>TC17147 Tobacco hairpin-Induced gene, HIN1<br>TC17482 Polykeide cyclase<br>TC04515 rNBC berls initiase VII.2<br>TC03515 MRC20Farting Totein Strates<br>TC03515 MRC20Farting Totein Minase MAP3KA<br>TC22585 United main-containing<br>TC03517 MRC50main potein RPM1<br>TC03485 STRUBBELIG-receptor family 3<br>TC14381 TObachila-receptor family 3<br>TC13485 TObachila-receptor family 3<br>TC13485 TObachila Factor 14<br>TC13481 TObachila Strates protein Strates<br>TC14381 TObachila Strates protein Strates<br>TC13451 Tobachila Strates protein domain-<br>TC13485 TObachila Freeptor family 3<br>TC13485 TOBachila Freeptor family 3<br>TC3455 Cytochrome p450 81F<br>TC03455 & Cytochrome p450 81F<br>TC03455 & Cytochrome p450 81F<br>TC03455 & TC15 & Spelot n   |   | Colorati WRRY 4<br>TC10233 MAP kinase kinase 5-like<br>TC02337 LRR and NB-ARC domains protein<br>TC146699 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC17285 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26148 Cys-rich receptor-kinase 7<br>TC05561 ADR1-LIKE 1<br>TC09291 ATP alpha hydrolases-like<br>TC03300 Cyclic nucleotide-gated ion channel 2<br>TC26148 Cys-rich receptor-kinase 7<br>TC05561 ADR1-LIKE 1<br>TC09291 ATP alpha hydrolases-like<br>TC03300 Co-NBS-LRR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32301 WRKY 46<br>TC03301 WRKY 46<br>TC03301 WRKY 46<br>TC03305 Receptor like protein 48<br>TC00918 Receptor like protein 48<br>TC009416 WRKY 31<br>TC22438 Suppressor OF npr1-1, SNC1<br>TC09483 Receptor like protein 48<br>TC00941 RAC/Perforin domain protein<br>TC23308 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC2071 Botrytis-susceptible1<br>TC02652 TIR-NBS-LRR protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Viclin-like antimicrobial peptides<br>TC04521 Bitte antimicrobial peptides<br>TC04521 Bitte antimicrobial peptides<br>TC04521 Cyclochrome p450 82C<br>TC18551 NBC1/HIN1-like 1, NHL1<br>TC10905 WRKY transcription stator 14<br>TC1716 Respiratory burst oxidase E like<br>TC27525 Glicochrome p450 825<br>TC21584 Cyclochrome p450 8381<br>TC27735 Lybechrome p450 8381<br>TC27785 Respiratory burst oxidase E like<br>TC27785 Prest cancer susceptibility protein 2<br>TC08685 MAjor latex protein like 25<br>TC17845 Polybeich Ninase 5.1-liko<br>TC27857 Bitte Contoin p450 8381<br>TC07857 Bitte Contoin DCF5.4-like<br>TC277955 Prest cancer susceptibility protein 2<br>TC08485 Lybe lectin kinase 5.1-liko<br>TC27857 ULP1-related protein domain-<br>TC1842 Polybeich Ninase MI2<br>TC17142 TP1-related protein domain<br>TC08380 MKL putative kinase, MAP3KA<br>TC22557 LURP1-related protein RPM1<br>TC19885 STRUBELIG-receptor-family 3<br>TC14381 TObarowius multigrication-like<br>TC32128 Cynodium-bitding receptor-kinase<br>TC32128 Cynodium-bitding receptor-kinase<br>TC3212                           |   | Colorati Nerky 4<br>TC (1076) NRRY 4<br>TC (1023) MAP kinase kinase 5-like<br>TC (1026) NRRY 4<br>TC (1023) MAP kinase kinase 5-like<br>TC (1023) Nitrilase 2<br>TC (1023) Nitrilase 2<br>TC (1023) Nitrilase 2<br>TC (1023) Nitrilase 2<br>TC (1025) Namorin Tamily protein<br>TC (1029) Namorin Namorina<br>TC (1029) Namorina Namorina<br>TC (1020) NAMA<br>TC (1020) |
| C | TC09644 Dirigent-like protein<br>TC02525 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRV411<br><b>SD-combined</b><br>TC07115 Vicilin-like antinicrobial peptides<br>TC014942 Reticuline oxidase-like<br>TC04521 Cytochrome p450 82C<br>TC04521 Cytochrome p450 82C<br>TC015851 Neclinine amidochansferase<br>TC04521 Cytochrome p450 82C<br>TC01920 Serifit protein fase 25<br>TC015851 NBC/HINI1-like 1, NHL1<br>TC01716 Respiratory burst oxidase Like<br>TC01920 Serifit protein fase 25<br>TC04585 Vicinome articotasterase 15<br>TC05955 United P450 82C<br>TC05955 United P450 825<br>TC04545 Lybe Icc1n kinase 25<br>TC04545 Lybe Icc1n kinase 5. I-like<br>TC05375 McCpeforin domain-containing<br>TC03575 McCpeforin domain-containing<br>TC03515 McCpeforin domain-containing<br>TC03515 McCpeforin domain-containing<br>TC03515 McClamabe Like RP451<br>TC121921 Paralog of NPR1<br>TC02587 Leibe ED10 Respirator 14<br>TC122857 LikeBELUG-receptor family 3<br>TC1381 Tobamovirus multiplication-like<br>TC32812 Cytochrome p450 81F<br>TC32825 Cytochrome p450 81F<br>TC32812 Cytochrome p450 81F   |   | Colorati MeRKY 4<br>TC (1023) MAP kinase kinase 5-like<br>TC (1076) MRKY 4<br>TC (1023) MAP kinase kinase 5-like<br>TC (1023) MAP kinase kinase 5-like<br>TC (1023) MAP dehydrogenase/GMP reductase<br>TC (1023) Mariane and the transformer of the<br>TC (1023) MAP alpha hydrolases-like<br>TC (1024) MAP alpha hydrolases for the<br>TC (1024) MAP alpha hydrolases for the fore alpha<br>TC (1024) MAP alpha hydrolases for the fore alpha hydrolases fore alpha hydrolases for the fore alpha hydrolase   |
| C | TC09644 Dirigent-like protein         TC02522 TIR-NBS-LRR protein         TC02522 TIR-NBS-LRR protein         TC026252 TIR-NBS-LRR protein         TC026923 Receptor like protein 48         TC21079 Cyclic nucleoside galdd channel 10         TC14520 WRKY41         State of the protein 20         TC01942 Retouline oxidase-like         TC3451 Dirigent-like antimicrobial peptides         TC01942 Retouline oxidase-like         TC3451 Dirigent-like protein 22         TC3451 Dirigent-like protein 22         TC3451 Dirigent-like protein 22         TC3451 Dirigent-like protein 22         TC34551 Oktohreme p450 82C         TC11851 NDRT/ININ-Like 1, NHL1         TC11920 Sertin protein knase 25         TC21736 Lipb lechrin knase 25         TC27736 Lipb lechrin knase 25         TC27736 Lipb lechrin knase 25         TC27736 Lipb lechrin knase 3         TC03493 FLyre Hordin knase VII.2         TC1744 Zno finger protein Klass VII.2         TC17442 Zno finger of the cyclase Billike         TC03830 MEX protein knase VII.2         TC1191 Paraiog of NPR1         TC11201 Paraiog of NPR1         TC11201 Paraiog of NPR1         TC11201 Paraiog of NPR1         TC11201 FL condexelor faming         TC3083   |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC17295 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC26148 Cys-rich receptor-kinase 7<br>TC05551 ADR-LIKE 1<br>TC039201 ATP alpha hydrolases-like<br>TC039201 ATP alpha hydrolases-like<br>TC039201 ATP alpha hydrolases-like<br>TC039201 CNBS-LRR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC322164 TIR-NBS-LRR class protein<br>TC322164 TIR-NBS-LRR class protein<br>TC32301 beaser resistance RPP13-like 3<br>TC00758 G-type lectin S-receptor kinase<br>TC03938 Diseaser resistance RPP13-like 3<br>TC00414 MKRY 31<br>TC22438 Suppressor OF np1-1; SNC1<br>TC0444 Mc/Perforin domain protein<br>TC23308 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein<br>TC29252 TR:NBS-LRR protein<br>TC20718 Dortylis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21078 (cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Vicilin-like antimicrobial peptides<br>TC01942 Reticuline oxidase-like<br>TC34213 Dirigent-like protein 22<br>TC24559 Glutanine amidotransferase<br>TC04511 Cytochrome p450 82C<br>TC14851 NDR1/HIN1-like 1, NHL1<br>TC19959 Glutanine amidotransferase<br>TC04517 Cytochrome p450 8381<br>TC095959 Glutanine amidotransferase<br>TC19959 Glutanine amidotransferase<br>TC19959 Glutanine amidotransferase<br>TC04571 Cytochrome p450 8381<br>TC09599 WRKY transcription factor 14<br>TC17114 Zine Inger protein DC5 4-like<br>TC27258 Lybe lectin kinase 25<br>TC19845 Major latex protein like 28<br>TC04945 Lybe lectin kinase 51-like<br>TC1742 Polykoide cyclase<br>TC03517 MAC/perforin domain-containing<br>TC03800 MRC putative kinase MI12<br>TC17842 Polykoide cyclase<br>TC03517 INS domain protein kinase B like<br>TC03517 INS domain protein RM11<br>TC11020 Paralog of NPR1<br>TC03204 Calterialina-Site<br>TC03205 Calterialina-Site<br>TC03205 Calterialina-Site<br>TC03205 Calterialina-Site<br>TC153205 Calterialina-Site<br>TC1532 |   | C10761 WRKY 4<br>TC10623 MAP kinase kinase 5-like<br>TC0233 TLR and N8-ARC domains protein<br>TC14669 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07499 Ser/Thr kinase, B120<br>TC17295 Remorin Tamily protein<br>TC02960 Cyclic nucleotide-gated ion channel 2<br>TC026148 Cyc-ich receptor-kinase 7<br>TC05551 ADR1-LIKE 1<br>TC03291 ATP aipha hydrolases-like<br>TC02920 CC-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32264 Supper lectin S-receptor kinase<br>TC0305 Sit-Inducible zistance RPP13-like 3<br>TC00758 G-type lectin S-receptor kinase<br>TC0993 Receptor like protein 48<br>TC00994 Receptor like protein 48<br>TC009416 WRKY 31<br>TC23308 ABA-responsive protein ABR18-like  |
| C | TC09644 Dirigent-like protein<br>TC02522 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleoside gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC01912 Reloculne oxidase-like<br>TC01912 Reloculne oxidase-like<br>TC01912 Reloculne oxidase-like<br>TC04517 Urdothme antimicrobial peptides<br>TC01925 Glutanine amidotransferase<br>TC04517 Cytochrome p450 82C<br>TC01982 Reloculne oxidase-like<br>TC09859 RHL/NIN1-like 1, NHL1<br>TC019716 Respiratory burst oxidase E like<br>TC09859 Glutary transcription Factor 14<br>TC19910 Sertify transcription Factor 14<br>TC17147 Tobacco hairpin-Indexd gane, HIN1<br>TC17845 Lybe lectin kinase VI.2<br>TC04957 ULRP1-reliatd protein CoT54-like<br>TC03957 ULRP1-reliatd protein domain-<br>TC03957 ULRP1-reliatd protein domain<br>TC03957 ULRP1-reliatd protein domain<br>TC03957 ULRP1-reliatd protein domain<br>TC03957 ULRP1-reliatd protein domain<br>TC03957 ULRP1-reliatd protein domain<br>TC1147 Tobacco hairpin-Indexd gane, HIN1<br>TC11201 Paragriatory burst oxidase B like<br>TC03957 ULRP1-reliatd protein domain<br>TC03957 ULRP1-reliatd protein domain<br>TC03958 STRUBELIG-receptor family 3<br>TC14381 Tobachulin- binding receptor-kinase<br>TC3282 SQtochrome p450 81F<br>TC03815 2 M-16 Reputerin<br>TC15828 Bak1-interacting receptor kinase 10<br>TC15828 Bak1-interacting receptor kinase<br>12<br>TC1848 Al-hook motf protein 20<br>TC1448 Reputering receptor-kinase<br>TC1848 STRUBELIG<br>TC1848 Reputering receptor-kinase<br>TC1848 Reputering receptor-kinase                    |   | CC10761 WRRY 4<br>TC10223 MAP kinase kinase 5-like<br>TC0233 TLR and NB-ARC domains protein<br>TC146691 IMP dehydrogenase/GMP reductase<br>TC16572 Dynamin-related protein 1E<br>TC11033 Nitrilase 2<br>TC0371 Receptor-like Ser/Thr kinase 10<br>TC07489 Ser/Thr kinase, B120<br>TC17285 Remorin family protein<br>TC02906 Cyclic nucleotide-gated ion channel 2<br>TC0551 ADR-1-LIKE 1<br>TC09291 ATP alpha hydrolases-like<br>TC03930 FC-NBS-LRR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32164 TIR-NBS-LLR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC32164 TIR-NBS-LRR class protein<br>TC323164 TIR-NBS-LRR class protein<br>TC32301 WRKY 46<br>TC03901 Receptor like protein 6<br>TC0444 MAC/Perforin domain protein<br>TC32308 ABA-responsive protein ABR18-like  |
|   | TC09644 Dirigent-like protein<br>TC28252 TIK-NBS-LRR protein<br>TC2071 Botrytis-susceptible1<br>TC09693 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC07115 Viclin-like antimicrobial peptides<br>TC09452 Rickulne oxidase-like<br>TC34530 Jingent-like protein 22<br>TC34530 Dirigent-like protein 22<br>TC34531 Dirigent-like protein 22<br>TC34531 Orgont-like noticase-like<br>TC34541 Cyclochrome p450 82C<br>TC18851 NDR1/HIN1-like 1, NHL1<br>TC10905 WRKY transcription starts<br>TC14542 Cyclochrome p450 8381<br>TC27736 Lype lectin kinase 5.1-like<br>TC27732 Breast cancer susceptibility protein 2<br>TC048451 Vytamiscription takes 2<br>TC14842 Oxford protein like 28<br>TC17424 Divelation containes 2.5<br>TC150380 MRKY transcriptions MI28<br>TC03390 MRK putative kinase 5.1-like<br>TC03390 MRK putative kinase 5.1-like<br>TC03390 MRK putative kinase MAP3KA<br>TC22857 LURP1-related protein domain-<br>TC11201 Paraiog of NRT1<br>TC12825 Pluster untilipication-like<br>TC32818 Tobamorius multipication-like<br>TC3288 Bak1-interacting receptor-kinase<br>TC3288 Bak1-interacting receptor RBR1<br>TC02828 Bak1-interacting receptor kinase 3.1-like<br>TC3288 Bak1-interacting receptor kinase<br>TC3288 Bak1-interacting receptor kinase<br>TC3288 Bak1-interacting receptor kinase 3.1-like<br>TC3288 Bak1-interacting receptor kinase 3.1-like<br>TC3288 Bak1-interacting receptor kinase 3.1-like<br>TC3288 Bak1-interacting receptor kinase 3.1-like<br>TC32878 Resistance to leptosphaeria maculans 3<br>TC04818 Cyrch receptor like kinase 10<br>TC13448 Receptor like protein 12<br>TC32848 TC18769 Resistance 2-like  |   | Control Trobanacio Characteria per la control per la control de la contr  |
| C | TC09644 Dirigent-like protein<br>TC02525 TIR-NBS-LRR protein<br>TC29071 Botrytis-susceptible1<br>TC09939 Receptor like protein 48<br>TC21079 Cyclic nucleotide gated channel 10<br>TC12755 Necrotic spotted lesions 1, NSL1<br>TC14620 WRKY41<br><b>SD-combined</b><br>TC09452 Reticuline oxidase-like<br>TC04521 Voltan-like antimicrobial peptides<br>TC04521 Voltan-like antimicrobial peptides<br>TC04521 Cytochrome p450 82C<br>TC01942 Reticuline oxidase-like<br>TC04521 Cytochrome p450 82C<br>TC019542 Reticuline antidoxale<br>TC04521 Cytochrome p450 82C<br>TC019542 Cytochrome p450 82C<br>TC019542 Cytochrome p450 83B1<br>TC09956 WRKY transcription Factor 14<br>TC17141 Zine finger protein factor 14<br>TC17141 Zine finger protein factor 14<br>TC17142 Delectrin kinase VII.2<br>TC04545 Lybe lectin kinase 2.5<br>TC04545 Lybe lectin kinase XII.2<br>TC04545 Lybe lectin kinase XII.2<br>TC04545 Lybe lectin kinase MIP3KA<br>TC03517 MRC2Perforin domain-containing<br>TC03517 MRC2Perforin domain-containing<br>TC03517 Protein Likase MIA<br>TC11201 Paralog of NPR1<br>TC13481 TOBAROW kinase MAP3KA<br>TC32804 Calreliculin-binding receptor-kinase<br>TC03415 CAlles Trobaro familio<br>TC13481 TOBAROW kinase MAP3KA<br>TC32824 Calreliculin-binding receptor-kinase<br>TC15426 B1/L-Receptor family 3<br>TC15484 Ah-hook motif protein 2<br>TC1485 Cys-rich receptor family 3<br>TC15482 B4/Linetracting receptor-kinase<br>TC15482 B4/Linetracting receptor-kinase<br>TC15482 B4/Linetracting receptor-kinase<br>TC15482 B4/Linetracting receptor family 3<br>TC15482 AA-hook motif protein 2<br>TC14442 Receptor protein kinase 2<br>TC14442 Receptor rike kinase 10<br>TC14442 Receptor rike kinase 10<br>TC14442 Receptor rike protein 12<br>TC13020 Receptor rike protein 12<br>TC13020 Receptor rike protein 12<br>TC13020 Receptor rike protein 12<br>TC13020 Receptor rike protein 1                     |   | Control Trobanacio Charlos per  |

#### F LD-combined

| I CU1716 Respiratory purst oxidase E like   |
|---|
| TC14139 Glutamine amidotransferase C13C5.04   |
| TC17114 Zinc finger protein Dof 5.4   |
| TC10920 Cvs-rich receptor kinase 25   |
| TC17958 Carboxylesterase 1 like   |
| TC08222 Loricio   |
| TC01750 KIP1-like   |
| TC04945 L tuga lactia kiaaca VII 2  |
| TC00404 Dessirates burst evidese D like   |
| TODED IO MAD Kinese 20  |
| TC25219 MAP Kinase 20   |
| TC06359 NAC domain containing protein 1   |
| TC03941 Alpha-trypsin inhibitor   |
| TC08744 CBL-interacting protein kinase 9  |
| TC24175 WRKY 47   |
| TC25350 WRKY 12   |
| TC22432 MAP kinase 3-like (MPK1)  |
| TC17147 Yellow-leaf-specific gene 9 like  |
| TC05119 MAP kinase MMK2-like  |
| TC22373 WRKY 33   |
| TC04889 TIR-NBS-LRR family protein  |
| TC03783 L ype lectin kinase S.5   |
| TC05415 Calmodulin-receptor kinase 2  |
| TC09799 Suppressor of npr1-1, SNC4  |
| TC12639 Avr9/Cf-9 rapidly elicited  |
| TC04229 Disease resistance protein RPM1   |
| TC04743 GMC oxidoreductase  |
| TC14525 HS1 PRO.1 2   |
| TC20044 Clucosul hudrolase with chitinase   |
| TC19011 Chiloseo 10   |
| TC14600 MIDKV 44  |
| TC00700 Teheses beigis induced case. UNIA   |
| TC09706 Tobacco nairpin-induced gene, HINT  |
| TC08606 Disease resistance RPP13-like 1   |
| TC11184 Cys, met, pro, gly protein 2, CMPG2   |
| TC16954 PR4a  |
|   |
| TC31840 Receptor-like ser/thr kinase 3  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17620 WRKY 75   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17620 WRKY 75<br>TC04922 Lysm receptor-like kinase  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochtinase-like<br>TC17820 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17620 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochtinase-like<br>TC17620 WRKY 75<br>TC04922 Uyem receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC04232 US5-LRR protein  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17820 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NB5-LRR protein<br>TC18618 Dirigent-like protein  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17620 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC04423 NB5-LRR protein<br>TC18418 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17820 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LRR protein<br>TC18618 Dirigent-like protein<br>TC18618 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like aprotein<br>10   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC15517 Acidic endochtinase-like<br>TC17620 WRKY 75<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 WRS-LRR protein<br>TC18418 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC04400 WRKY 72   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17520 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LRR protein<br>TC18618 Dirigent-like protein<br>TC0400 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC1517 Actic endochtinase-like<br>TC17620 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LR protein<br>TC04618 Dingent-like protein<br>TC04618 Dingent-like protein<br>TC04613 Inceptor-like ser/thr kinase 10<br>TC04603 Inceptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reticuline oxidase-like   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC105472 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC17232 WRKY 31<br>TC06423 NBS-LRR protein<br>TC18618 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72   |
| TC31840 Receptor-like ser/thr kinase 3           TC05374 VAK-LIKE 10           TC10517 Ackic endochitinase-like           TC1720 WRKY 75           TC34526 Defensin (AFP) gene           TC17220 WRKY 31           TC04222 NBS-LRR protein           TC1820 Original Streeptor-like kinase           TC34554 Defensin (AFP) gene           TC17220 WRKY 31           TC06422 NBS-LRR protein           TC04032 Clayber-like protein           TC04030 Claybe lectin S-receptor kinase           TC04030 Clayber lectin S-receptor kinase 10           TC34400 WRKY 72           TC04030 Clayber lectin S-receptor kinase 10           TC34400 WRKY 72           TC04030 Clayber lectin S-receptor kinase 10           TC34400 WRKY 72           TC04030 Clayber lectin S-receptor like protein 7           TC14148 Receptor-like ser/thr kinase 10           TC34400 WRKY 72           TC04030 Clayber lectin S-receptor like protein 7           TC14148 Receptor like protein 7   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17220 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC04428 NB5-LRR protein<br>TC04428 NB5-LRR protein<br>TC046181 Dirigent-like protein<br>TC046181 Dirigent-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reticuline oxidase-like<br>TC14148 Receptor-like protein 7<br>TC12020 Hevin chitinase<br>TC3400 WRKY 72<br>TC12020 Hevin chitinase<br>TC3400 WRKY 72<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37<br>TC37 |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17520 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LRR protein<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reticuline oxidase-like<br>TC14148 Receptor like protein 7<br>TC1220 Hevein chitinase<br>TC24032 Endochitinase PR4-like<br>TC24032 Werkin 22  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochtinase-like<br>TC17220 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC0423 NBS-LRR protein<br>TC18418 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reliculine oxidase-like<br>TC14148 Receptor like protein 7<br>TC12020 Hevin chitinase<br>TC24032 Endochtinase PR4-like<br>TC2409 WRKY 72<br>TC20690 Xevin chitinase   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17200 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LRR protein<br>TC18618 Dirigent-like protein<br>TC18618 Dirigent-like protein<br>TC04006 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reticuline oxidase-like<br>TC14148 Receptor like protein 7<br>TC12202 Hevein chitinase<br>TC24032 Endochitinase PR4-like<br>TC24039 WRKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC3241.7-hook modif protein 15  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC15517 Actic endochtinase-like<br>TC17620 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17229 WRKY 31<br>TC06423 NBS-LRR protein<br>TC16818 Dingent-like protein<br>TC0406 CHype lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC069902 Reticuline oxidase-like<br>TC14146 Receptor like protein 7<br>TC120201 Hevein chilinase<br>TC24032 Endochtinase PR4-like<br>TC24021 WerKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC24821 AT-hook motif protein 15<br>TC2495 Chilin2 chilinase  |
| TC31840 Receptor-like ser/thr kinase 3         TC05374 WAK-LIKE 10         TC17230 WRXY 75         TC37520 WRXY 75         TC34526 Defensin (AFP) gene         TC34524 Defensin (AFP) gene         TC17223 WRXY 31         TC04822 Lyss receptor-like kinase         TC17825 WRXY 31         TC049242 NBS-LRR protein         TC1818 Dipigent-like protein         TC04962 Reticuline ser/thr kinase 10         TC34400 WRXY 72         TC04962 Reticuline sovidase-like         TC14146 Receptor Like protein 7         TC12202 Hevein chinase         TC24032 Endochkinase PR4-like         TC20199 WRXY 72         TC31019 Malectin/receptor-like kinase         TC23217 AT-hook motif protein 15         TC2397 Chin2 chinase         TC2397 FX147-arage GT4-binding protein 1  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC1517 Actic endochitinase-like<br>TC17620 WRKY 75<br>TC47620 WRKY 75<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LR protein<br>TC0406 C+ype lectin S-receptor kinase<br>TC04511 Receptor-like protein<br>TC04061 C+ype lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reticuline oxidase-like<br>TC14148 Receptor like protein 7<br>TC12020 Hevein chitinase<br>TC24512 Export Interprotein 15<br>TC26079 WRKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC2871 Art-large GTP-binding protein 1<br>TC2957 Extra-large GTP-binding protein 1   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC1720 WRXY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRXY 31<br>TC06423 NB5-LRR protein<br>TC18618 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase<br>TC0451 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC05902 Reticuline oxidase-like<br>TC14148 Receptor like protein 7<br>TC12020 Hevein chitinase<br>TC24032 Endochitinase PR4-like<br>TC24032 ChatChitinase PR4-like<br>TC2009 WRXY 72<br>TC23019 Multechitreceptor-like kinase<br>TC23271 AT-hook motif protein 15<br>TC23027 Chitina 2-hitinase<br>TC32957 Chitina 2-hitinase<br>TC3878 Restance to Jeptosphaeria maculans 3  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC1517 Actic endochitinase-like<br>TC17620 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17220 WRKY 31<br>TC064023 NBS-LRR protein<br>TC0400 G-type lectin S-receptor kinase<br>TC04108 Teceptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06902 Reticuline oxidase-like<br>TC14148 Receptor-like ser/thr kinase 10<br>TC24032 Endochitase<br>TC24032 Endochitase PR4-like<br>TC24030 WRKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC2871 Art-hook motif protein 15<br>TC28271 Art-hook motif protein 15<br>TC28275 Chitina 2-thitase<br>TC18997 Extra-large GTP-binding protein 1<br>TC05650 Botrytis-susceptible 1<br>TC13195 Servitr kinase PR45   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC17820 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LRR protein<br>TC18618 Dirigent-like protein<br>TC0406 G-type lectin S-receptor kinase<br>TC0451 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06902 Refuculine oxidase-like<br>TC14148 Receptor like protein 7<br>TC12402 Hevein chitinase<br>TC24032 Endochitinase PR4-like<br>TC24032 Proto-hitinase<br>TC23019 MRKY 72<br>TC2099 WRKY 72<br>TC23019 Watch 2 chitase<br>TC28271 AT-hook motif protein 15<br>TC2957 Chita 2 chitase<br>TC18788 Resistance to leptosphaeria maculans 3<br>TC31139 Ser/thr kinase PR5K  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC105372 Ackicle endochitinase-like<br>TC17520 WRKY 75<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NBS-LRR protein<br>TC0468 E-type lectin S-receptor kinase<br>TC045611 Receptor-like protein<br>TC0468 E-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC069802 Reticuline oxidase-like<br>TC14148 Receptor-like kinase<br>TC2452 Endochitinase PR4-like<br>TC22079 WRKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC2857 Chitin2 chitinase<br>TC1897 Extra-large GTP-binding protein 1<br>TC0595 Bottylis-susceptble1<br>TC18978 Resistance to leptosphaeria maculans 3<br>TC31395 Ser/thr kinase PR5K<br>TC1358 Endochitinase   |
| TC31840 Receptor-like ser/thr kinase 3<br>TC0537 VMxL-IKE 10<br>TC10517 Acidic endochitinase-like<br>TC17820 WRKY 75<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06423 NB5-LRR protein<br>TC0406 G-type lectin S-receptor kinase<br>TC0451 Receptor-like servith kinase 10<br>TC34400 WRKY 72<br>TC069062 Reticuline oxidase-like<br>TC14148 Receptor like protein 7<br>TC12402 Hevein chinase<br>TC24032 Endochinase PR4-like<br>TC24032 Endochinase PR4-like<br>TC205079 WRKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC28271 AT-hook motif protein 15<br>TC2957 Chin2 chinase PR4-like<br>TC18789 Resistance to leptosphaeria maculans 3<br>TC31395 Ser/thr kinase PR5K<br>TC11738 Endochinase PR5K<br>TC13030 Receptor like protein 7<br>TC13030 Receptor like<br>TC13030 Receptor like<br>TC13030 Receptor like<br>TC13030 Receptor like protein FLS2  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC105372 Ackicle endochitinase-like<br>TC17220 WRKY 75<br>TC04922 Lysm receptor-like kinase<br>TC34554 Defensin (AFP) gene<br>TC17220 WRKY 31<br>TC06423 NBS-LRR protein<br>TC0406 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC06962 Reticuline oxidase-like<br>TC14148 Receptor-like ser/thr kinase 10<br>TC24020 Hevein chitinase<br>TC24032 Endochitinase PR4-like<br>TC28079 WRKY 72<br>TC31019 Malectin/receptor-like kinase<br>TC2871 AT-hook motif protein 15<br>TC28271 AT-hook motif protein 15<br>TC28271 AT-hook motif protein 15<br>TC18997 Extra-large GTP-binding protein 1<br>TC05950 Botrytis-susceptible 1<br>TC18987 Extra-large GTP-binding protein 1<br>TC18987 Setsitance to leptosphaeria maculans 3<br>TC31395 Ser/thr kinase PR5K<br>TC11375 Hevamine-A-like  |
| TC31840 Receptor-like ser/thr kinase 3<br>TC05374 WAK-LIKE 10<br>TC10517 Acidic endochitinase-like<br>TC134574 Acidic endochitinase-like<br>TC34554 Defensin (AFP) gene<br>TC34554 Defensin (AFP) gene<br>TC17223 WRKY 31<br>TC06422 NBS-LRR protein<br>TC0400 G-type lectin S-receptor kinase<br>TC04511 Receptor-like ser/thr kinase 10<br>TC04501 Receptor-like ser/thr kinase 10<br>TC34400 WRKY 72<br>TC09992 Reticuline oxidase-like<br>TC14148 Receptor like protein 7<br>TC12402 Hevein chitinase<br>TC24032 Redochitinase PR4-like<br>TC24032 Chardonhitinase PR4-like<br>TC24032 Chardonhitinase PR4-like<br>TC24032 Filter Chitinase<br>TC24032 Filter Chitinase<br>TC24032 TC11708 Endochitinase PR4-like<br>TC26050 BWRKY 72<br>TC1999 PXtra-large GTP-binding protein 1<br>TC19997 Extra-large GTP-binding protein 1<br>TC19550 Bottylis-susceptbela1<br>TC11738 Resistance to leptosphaeria maculans 3<br>TC31395 Ser/thr kinase PR5K<br>TC13030 Receptor Like protein FLS2<br>TC13030 Receptor Like protein FLS2<br>TC13030 Receptor Like protein FLS2<br>TC13030 Receptor Like protein FLS2  |

FIGURE 7 | Expression profile of genes involved in defense responses under individual and combined stress transcriptome. DEGs with minimum fold change 1 (Log<sub>2</sub> converted) were identified in each individual and combined stressed plants over their respective controls. DEGs involved in defense responses were identified using MAPMAN software and literature survey. Heat map represent expression profile of 'defense response related' genes under SD-pathogen (A), SD-drought (B), SD-combined (C), LD-pathogen (D), LD-drought (E), and LD-combined stresses (F). Fold change values (over respective controls) are represented in heat maps where color bar in red and blue represents up- and down-regulated genes, respectively.

drought stress like effect. Xylem invading *Xylella fastidiosa* was also found to invoke drought like response as it upregulated expression ABA biosynthesis genes and two galactinol synthase genes involved in synthesis of galactinol and raffinose osmoprotectants (Choi et al., 2013).

The transcriptomic changes under SD-combined stress in this study directed toward defense response mediated SA and ET signaling and lignin and flavonoid accumulation. Contrastingly, LD-combined stress showed repressed expression of SA and ET signaling genes along with various defense related genes and thus induced the susceptibility of plant. We noted differential expression of various genes unique to SD- and LD-combined stresses. One of the unique responses under SD-combined stress was specific up-regulation of ET signaling gene Multiprotein Bridging Factor-1c (MBF1c). MBF1 is a DNA-binding protein transcriptional coactivator which is involved in regulating metabolic and development pathways (Suzuki et al., 2011). Earlier, up-regulation of MBF1c was noticed in A. thaliana under pathogen infection, salinity, drought, heat, hydrogen peroxide, ABA, and SA application (Rizhsky et al., 2004; Tsuda and Yamazaki, 2004). Moreover, its constitutive expression was reported to increase the tolerance of transgenic plants to bacterial infection, salinity, heat, and osmotic stress and combined heat and osmotic stress (Suzuki et al., 2005). Similarly, genes encoding for auxin receptor TIR, transporters ABCB4, HP4, ARR17, PXY, and SND2 showed up-regulation only under SD-combined stress.

Xylem being conductor of water in plant is the most affected tissue under drought (De Souza et al., 2013) and wilt diseases (Yadeta and Thomma, 2013). While inhabiting the xylem, vascular pathogen exploits all inorganic and sugar resources present in the xylem (Yadeta and Thomma, 2013). Also, it enzymatically digests xylem cell wall to fulfill its nutritional needs (Yadeta and Thomma, 2013). The plant in turn, induces vascular coating as well as metabolic changes like secretion of PR proteins, peroxidases, proteases, xyloglucan-endotransglycosylase (XET), and xyloglucan-specific endoglucanase inhibitor protein (XEGIP), phenols, phytoalexins, and lignin-like compounds as a part of the plant defense toward the pathogen (Yadeta and Thomma, 2013). Primary and SCW also modulate ET, JA, SA, and ABA hormone signaling and thus have role in drought stress tolerance and regulation of defense response (Schulze-Lefert, 2004; Somerville et al., 2004; Hernández-Blanco et al., 2007; Denancé et al., 2013). In this regard, we looked for the expression of genes involved in xylem differentiation and SCW modification to understand if plant is utilizing xylem modification or re-differentiation as defense mechanism against combined stress. We observed that SDcombined stress had up-regulated expression of genes involved in xylem differentiation and SCW modification especially genes involved in lignin biosynthesis. During LD-combined stress the genes involved in cellulose biosynthesis were up-regulated. Increased lignin accumulation has been shown to increase the plants defense mechanism (Bhuiyan et al., 2009; Xu et al., 2011). However, on contrary increased cellulose synthesis is known to

increase the susceptibility of plants toward pathogen. Hernández-Blanco et al. (2007) showed that mutation in cellulose synthase encoding genes (*CeSA4*, *CeSA7*, and *CeSA8*) for cellulose deposition in SCW enhanced resistance of *A. thaliana* toward *R. solanacearum*. In our study, we could partly correlate increased lignification during SD-combined stress with the enhanced defense under this stress and up-regulation of *CeSA7* with the compromised disease resistance in LD-combined stressed plants.

## CONCLUSION

The study highlights that combined drought and *R. solanacearum* stress invokes transcriptome changes unique to combined stress and also transcriptome common between combined and individual stresses in chickpea. SD-combined stress in chickpea causes up-regulation of genes involved in SA, ET signaling, and lignin biosynthesis. LD-combined stress down-regulates the expression of defense related genes and increases expression of genes involved in cellulose biosynthesis resulting in susceptibility of chickpea toward *R. solanacearum*. Transcriptome under *R. solanacearum* infection exhibit up-regulated expression of various abiotic stress related genes and displays closeness with the SD-combined stress transcriptome.

## **AUTHOR CONTRIBUTIONS**

MS-K conceived the idea. MS-K and RS designed the study. RS and AG performed the experiments. RS analyzed the data with the input from MS-K. MS-K and RS wrote the manuscript.

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## SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: http://journal.frontiersin.org/article/10.3389/fpls.2017.00333/ full#supplementary-material

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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